

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of: Kenneth Rhodes *et al.*

Serial No.: N/A

Filed: Herewith

For: *POTASSIUM CHANNEL INTERACTORS AND
USES THEREFOR*

Attorney Docket No.: MNI-070CP4

Assistant Commissioner for Patents
Box Sequence
Washington, D.C. 20231

TRANSMITTAL LETTER FOR DISKETTE CONTAINING SEQUENCE LISTING

Dear Sir:

Enclosed is a diskette which contains a computer readable form of the Sequence Listing for the patent application filed herewith. The Sequence Listing complies with the requirements of 37 C.F.R. § 1.821. The material on this diskette is identical in substance to the sequence listing appearing on pages 1-92 of the Sequence Listing which is submitted herewith, as required by 37 C.F.R. § 1.821(f). The computer readable form of the Sequence Listing contained on the enclosed diskette is understood to comply with the requirements of § 1.824(d).

"Express Mail" mailing label number EI 011 360 044 US

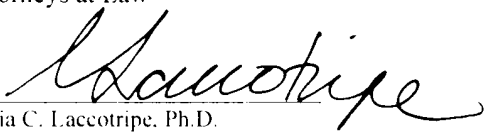
Date of Deposit September 27, 2000

I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to the Assistant Commissioner for Patents, Box Sequence, Washington, D.C. 20231

Nelson Barros
Signature

Nelson F. Barros
Please Print Name of Person Signing

LAHIVE & COCKFIELD, LLP
Attorneys at Law

By 
Maria C. Laccotripe, Ph.D.
Agent for Applicants
Limited Recognition Under 37 C.F.R. §10.9(b)
28 State Street
Boston, MA 02109
Telephone: 617-227-7400
Facsimile: 617-742-4244

REFERENCE LISTING

<11> Rhodes, Kenneth
Perry, Maria
Lilly, Heidi-Pink
An, Wenqian

<120> POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR

<130> MN1-070CP4

<140>

<141>

<150> USSN 60/110,277

<151> 1998-11-30

<150> USSN 60/110,033

<151> 1998-11-25

<150> USSN 60/109,333

<151> 1998-11-10

<150> USSN 09/198,731

<151> 1999-04-23

<150> USSN 09/180,614

<151> 1999-07-09

<150> USSN 09/180,874

<151> 1999-07-09

<150> USSN 09/400,492

<151> 1999-09-21

<150> USSN 09/399,913

<151> 1999-09-21

<150> PCT/US99/27428

<151> 1999-11-19

<160> 73

<170> International Ver. 2.1

<210> 1

<211> 1463

<212> DNA

<213> Homo sapiens

<220>

SEQUENCE LISTING (Table 1) CONTAINS THE SEQUENCE INFORMATION FOR THE INVENTION

SEQUENCE LISTING (Table 1) CONTAINS THE SEQUENCE INFORMATION FOR THE INVENTION

atg ggc acc ttc tca tct ctg caa acg aaa cag agg gga tgg tgg aaa 10
Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg Arg Pro Ser Lys

5 10 15 20

GAT AAG ATT GAA GAT GAG CTG GAG ATG ACC ATG GTT TTT GAT GGG ACC 332
 Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys His Arg Pro
 25 30 35

gag gga ctg gag cag ctg gag gcc sag acc aac ttc acc aag agg gag 380
Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg Glu
40 45 50

ctg cag gtc att tat cga ggc ttc aaa aat gag tgc ccc agt ggt gtg 428
Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val
55 60 65

gtc aac gaa gac aca ttc aag sag atc tat gct sag ttt ttc gct cat 476
Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His
70 75 80

gga gat gcc agc aag tat gcc cat tac ctg ttg aat gcc ttg gac aac 524
Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr
85 90 95 100

act cag aca ggc tcc gtg aag ttc gag gac ttt gta acc gct ctg tgg 572
Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser
105 110 115

att tta ttg aga gga act gtc cac gag aaa cta agg tgg aca ttt aat 620
Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn
120 125 130

ttg tat gac atc aac aag gac gga tac ata aac aaa gag gag atg atg 668
Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met
135 140 145

jac att gtc aaa ggc atc tat gag att atg ggg aaa tac aca tat cct 716
 Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro
 160 161 162

gtg etc aaa gag gac aat cca agt cag cat gtg gac gta ttc ttc cag 764
Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln
165 170 175 180

144 Met Asp Lys Asp Lys Asp Glu Ile Val Thr Leu Asp Phe Phe Leu
145 Met Asp Lys Asp Lys Asp Glu Ile Val Thr Leu Asp Phe Phe Leu

[illegible]

taattattat taattattat taattattat taattattat taattattat 1170
 taggaataga taattattat taattattat taattattat taattattat 1180
 taattattat taggaataga taattattat taattattat taattattat 1190
 agaaataga taattattat taggaataga taattattat taattattat 1152
 atggaaatga taattattat taattattat taattattat taattattat 1212
 taattattat taattattat taattattat taattattat taattattat 1272
 taattattat taattattat taattattat taattattat taattattat 1332
 taggaataga taattattat taattattat taattattat taattattat 1392
 taattattat taattattat taattattat taattattat taattattat 1452
 taattattat taattattat taattattat taattattat taattattat 1463

```
<210> 1
<211> 16
<212> PRT
<213> Homo sapiens
```

```

0400> 1
Met Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg
  1              5              10              15
Arg Pro Ser Lys Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val
              20              25              30
Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
              35              40              45
Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
  50              55              60
Pro Ser Gly Val Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln
  65              70              75              80
Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
              85              90              95
Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
              100              105              110
Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Gln Lys Leu Arg
              115              120              125

```

Val Ile Ile Val Lys Met Asp Lys Asn Lys Asp Lys Ile Val Thr Leu
171 173 175

Asp Glu Ile Leu Val Ser Cys Glu Glu Asp Asp Asn Ile Met Arg Ser
180 182 184

Leu Glu Leu Phe Glu Asn Val Met
210 215

<210> 3

<211> 1856

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (300)..(1034)

<400> 3

ggcacaac cctggattc ttgggagaat atgcctgag gtgttgccaa ttattagttc 60

tcttggetag cagatgttta gggaactggtt aagcctttgg agaaattacc ttaggaaaac 120

ggggaaataa aagcaagat taccatgaat tgcaagatta cctagcaatt gcaaggtagg 180

aggagagagg tggagggcgg agtagacagg agggagggag aaagtgagag gaagctaggc 240

tggtggaat aacctgcac ttggaacagc ggcaagaag cgcgattttc cagctttaa 299

atg cct gcc ggc ggt ctg ctt gcc tac cgg gga acg gag atg ttg acc 347

Met Pro Ala Arg Val Leu Leu Ala Tyr Pro Gly Thr Glu Met Leu Thr
1 5 10 15

cag gcc gag tct gaa ggg ctc cag acc ttg ggg ata gta gtg gtc ctg 395

Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu
20 25 30

tgt tcc tct ctg aaa cta ctg cac tac ctc ggg ctg att gac ttg tgg 443

Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
35 40 45

gat gac aac atc gat gat gat ctg gat atc atc atc atc atc atc atc 491

Asp Asp Lys Ile Gln Asp Asp Leu Ala Met Thr Met Val Cys His Arg
50 55 60

cct gag gga ctg gag cag ctt gag gca cag acg aac ttc acc aag aga 539

Pro Gln Gly Leu Gln Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg
65 70 75 80

TAT TAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT GAT 601

Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr Ala Gln Phe Phe Pro
100 105 110 115 120

Glu Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Arg His His
 210 215 220

0111-1111
 0111-1111
 0111-1111

0111-1111
 0111-1111
 0111-1111 (1124)

0400> 5

agggcccccctg agatccagcc ccagcccgccg ggggagggcc cgggtggccg cggggggggg 60
 cggggg-gagg gcagatcccg ccagccagcc gggggggg cggcagccgc ggggtgggg 120
 gcagcccgcc cccgtgtcca acatccagcca ggttttgggg cgggggggc ggggtggga 180
 gaagccagtg gcccggctgg gtcccagcc cggggggggc ctgtgaagcc cccggcagc 240
 ctctggccct gggagtcagt gcctgtgctt ggtgaagaa ggcagcagcc acgagctcca 300
 gggcccccgg ccccaagttt tctgaatacc aagctgcagg ccagctgctc ggggtttttt 360
 tggttctctg cttttctctt cctccaattc aaagtgggca atccacaccg atttcttttc 420
 aggggagggg agagacaggg cctgggggtc caagacgcac acaagtcttc gctgcc atg 479
 Met
 1

ggg gcc gtc atg ggc act ttc tcc tcc ctg cag acc aaa caa agg cga 527
 Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg Arg
 5 10 15

ccc tct aaa gac aag att gag gat gag cta gag atg acc atg gtt tgc 575
 Pro Ser Lys Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys
 20 25 30

cac cgg cct gag gga ctg gag cag ctt gag gca cag acg aac ttc acc 623
 His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr
 35 40 45

aag aga gaa ctg caa gtc ttg tac cgg gga ttc aaa aac gac tgc cct 671
 Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro
 50 55 60 65

acc ccc ccc ccc att gaa gaa gaa ttc aag gag att tac gct cag ttt 719
 Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe
 70 75 80

ttc cct cac gga gat gcc agc aca tat gaa cat tat ctc ttc aat acc 767
 Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala
 85 90 95

acc ccc ccc ccc att gaa gaa gaa ttc aag gag att tac gct cag ttt 807
 Ala Leu Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe
 100 105 110

101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- 210 - 6

[illegible]

[illegible]

```
<210> 7
<211> 1534
<212> DNA
<213> Rattus sp.
```

```
<220>
<221> CDS
<222> (31)..(711)
```

<400> 7

Met Gly Ala Val Met Gly Thr Phe

[illegible]

cctacgacga tagaacaagt ctttaaacac atcaggagg gaaacccgtg cccagtggtc 1391
 tatcccttct ctcacatccc tgcacaagcc cagcaatgca tgcctctccc ggaaggttca 1451
 gaatgcctgt gaaatgcctt aacttttata cccgtttata atcaataaac agaactattc 1511
 cgtacaaaaa aaaaaaaaaa aaa 1534

<210> 8

<211> 227

<212> PRT

<213> Rattus sp.

<400> 8

Met	Gly	Ala	Val	Met	Gly	Thr	Phe	Ser	Ser	Leu	Gln	Thr	Lys	Gln	Arg
1				5						10					15
Arg	Pro	Ser	Lys	Asp	Ile	Ala	Trp	Trp	Tyr	Tyr	Gln	Tyr	Gln	Arg	Asp
			20					25					30		
Lys	Ile	Glu	Asp	Asp	Leu	Glu	Met	Thr	Met	Val	Cys	His	Arg	Pro	Glu
		35					40					45			
Gly	Leu	Glu	Gln	Leu	Glu	Ala	Gln	Thr	Asn	Phe	Thr	Lys	Arg	Glu	Leu
	50					55					60				
Gln	Val	Leu	Tyr	Arg	Gly	Phe	Lys	Asn	Glu	Cys	Pro	Ser	Gly	Val	Val
65					70					75					80
Asn	Glu	Glu	Thr	Phe	Lys	Gln	Ile	Tyr	Ala	Gln	Phe	Phe	Pro	His	Gly
				85					90					95	
Asp	Ala	Ser	Thr	Tyr	Ala	His	Tyr	Leu	Phe	Asn	Ala	Phe	Asp	Thr	Thr
			100					105					110		
Gln	Thr	Gly	Ser	Val	Iyr	Phe	Gln	Arg	Phe	Val	Thr	Ala	Leu	Ser	Ile
		115					120					125			
Leu	Leu	Arg	Gly	Thr	Val	His	Glu	Lys	Leu	Arg	Trp	Thr	Phe	Asn	Leu
	130					135					140				
Tyr	Asp	Ile	Asn	Lys	Asp	Gly	Tyr	Ile	Asn	Lys	Glu	Gln	Met	Met	Asp
145															
Leu	Lys	Ala	Arg	Ile	Leu	Arg	Ala	His	Val	Arg	Val	Leu	Phe	Ala	Lys
	155							160					165		

Ser Tyr Val Val Asp Arg Asn Ile Met Asn Ser Leu Val Leu Ile Val
 215 216 217

Asn Val Met
 218

<210> 9
 <211> 1343
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (77)..(757)

<400> 9
 atccacaccg attttttttt aggggagggg agagacaggg cctgggggtcc caagaacgac 60
 acaagtcttc gctgcc atg ggg gcc gtc atg ggc act ttc tcc tcc ctg cag 112
 Met Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gln
 1 5 10
 acc aaa caa agg cga ccc tct aaa gac atc gcc tgg tgg tat tac cag 160
 Thr Lys Gln Arg Arg Pro Ser Lys Asp Ile Ala Trp Trp Tyr Tyr Gln
 15 20 25
 tat cag aga gac aag att gag gat gag cta gag atg acc atg gtt tgc 208
 Tyr Gln Arg Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys
 30 35 40
 cac cgg cct gag gga ctg gag cag ctt gag gca cag acg aac ttc acc 256
 His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr
 45 50 55 60
 aag aga gaa ctg caa gtc ttg tac cgg gga ttc aaa aac gag tgc cct 304
 Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro
 65 70 75
 agc ggt gtg gtc aat gaa gaa aca ttc aag cag atc tac gct cag ttt 352
 Ser Gly Val Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe
 80 85 90
 ttc cct cct cca tat gtt ggt ggt tat ggt tat ggt tat ggt tat ggt 400
 Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala
 95 100 105
 ttc gac acc acc cag aca ggc tct gta aag ttc gag gac ttt ctt act 448
 Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr
 110 115 120
 ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 480
 Thr Phe Asn Leu Tyr Arg Ile Asn Lys Arg Gly Tyr Ile Asn Lys Thr
 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200

Ala Val Leu Tyr Arg Ile Ala Thr Tyr Tyr Tyr Ile Tyr Glu Asn Asn

Lys Leu Ala Asp Val Leu His Met Thr Met Val Cys His Arg Leu His
4 4

Lys Leu Glu Glu Leu Glu Ala Glu Thr Asn Phe Thr Lys Arg Glu Leu
5 5

Gln Val Leu Tyr Arg Gly Ile Lys Asn Glu Cys Pro Ser Gly Val Val
6 6

Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His Gly
85 90 95

Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr Thr
100 105 110

Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser Ile
115 120 125

Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn Leu
130 135 140

Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met Asp
145 150 155 160

Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Val
165 170 175

Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln Lys
180 185 190

Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe Leu Glu
195 200 205

Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu Phe Gln
210 215 220

Asn Val Met
225

<210> 11
<211> 955
<212> DNA
<213> Rattus sp.

<220>
<221> CDS
<222> (345)..(953)

<220>
<223> Xaa at position 92 of the corresponding amino acid
sequence may be any amino acid

<210> 1
 <211> 181
 <212> Homo sapiens

<213> 1

Met Leu Thr Gln Gly Gln Ser His Gly Leu Gln Thr Leu Gly Ile Val
 1 5 10 15

Val Val Leu Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile
 20 25 30

Asp Leu Ser Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val
 35 40 45

Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
 50 55 60

Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
 65 70 75 80

Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Xaa Ile Tyr Ala Gln
 85 90 95

Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
 100 105 110

Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
 115 120 125

Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys
 130 135 140

Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
 145 150 155 160

Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
 165 170 175

Tyr Thr Tyr Leu Val Leu Lys Glu Asp Thr Ser Arg Gln His Val Asp
 180 185 190

Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp
 195 200

<210> 1
 <211> 2009
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

2009 2009 2009 2009

2009 2009 2009 2009

2009 2009 2009 2009 2009 2009 2009 2009 2009 2009

2009 2009 2009 2009 2009 2009 2009 2009 2009 2009

Met Arg Arg Ala Gly Arg Lys Ala Ser
1

ttt tcc gat ttc taa tat ctg gac agc ttt tat tat tat ttc acc ggt 241
Leu Ser Asp Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly
15 16 19 25

cac cct cca ggg ccc act aaa aaa ggg ctg aag cag cga ttc ctg aag 329
His Pro Pro Gly Pro Thr Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys
30 35 40

ctg ctg cgg tgc tgc ggg ccc caa gcc ctg ccc tca gtc agt gaa aca 377
Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Thr
45 50 55

tta gcc gcc cca gcc tcc ctg cgc ccc cac aga ccc cgc ctg ctg gac 425
Leu Ala Ala Pro Ala Ser Leu Arg Pro His Arg Pro Arg Leu Leu Asp
60 65 70

cca gac agc gtg gac gat gaa ttt gaa ttg tcc acc gtg tgt cac cgg 473
Pro Asp Ser Val Asp Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg
75 80 85

cct gag ggt ctg gag cag ctg cag gag caa acc aaa ttc acg cgc aag 521
Pro Glu Gly Leu Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Lys
90 95 100 105

gag ctg cag gtc ctg tac cgg ggc ttc aag aac gaa tgt ccc agc gga 569
Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
110 115 120

att gtc aat gag gag aac ttc aag cag att tac tcc cag ttc ttt cct 617
Ile Val Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro
125 130 135

caa gga gac tcc agc acc tat gcc act ttt ctg ttc aat gcc ttt gac 665
Gln Gly Asp Ser Ser Thr Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp
140 145 150

acc aac cat gat ggc tgg gtc agt ttt gaa aac ttc gtc gct ggt ttg 713
Thr Asn His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu
155 160 165

tct gtt att ttt gtt gtt att gta tat tat agt ttt gtt tgg gtc ttc 761
Ser Val Ile Leu Arg Gly Thr Val Asp Asp Arg Leu Asn Trp Ala Phe
170 175 180 185

aac ctg tat gac ctt aac aag gac ggc tgc atc acc aac aac gaa atg 809
Asn Leu Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Gln Gln Met
190 195 200

[illegible]

1001
 116 Gln Ser Cys Gln Lys Arg Glu Asn Ile Met Arg Ser Met Glu Leu
 250 251 260 265

tit gac aat gtc atc tagccccag gagaggggt cagtggttcc tggggggacc 1056
Phe Asp Asn Val Ile
270

atggtctctaac	cctagttccag	ggggacctca	cccttctctt	cccaggtctc	tctctctctt	1116
acgcctctct	ggggggtgga	gggatccaa	agcttgggga	ttcagtagtc	cagatctctg	1176
gagctgaagg	ggccagagag	tgggcagagt	gcctctctgg	gggtgttccc	aaatcccacc	1236
agctctcacc	cccttctctg	ctgacaccca	gtgttgagag	tgcctctctt	gtaggaattg	1296
agcgggtccc	caactctctc	cctactctag	aaacacacta	gagcgatgtc	tctgtctatg	1356
gtgcttcccc	cctccctgac	ctcctaaaca	tttcccctaa	gactccctct	tcagagagaa	1416
tgtccctctc	ttgggactgg	ctgggtctct	agaccagcca	ttgagagccc	tgtgggaggg	1476
ggacaagaat	gtatagggag	aaatcttggg	cctgagtcac	tggatagggt	ctaggagggt	1536
ggtgggggtg	agaatagaag	ggcctggaca	gattatgatt	gtccaggcat	accagggtat	1596
agctccaagt	tcacacaggt	tgtaccaca	ggccatcaaa	atataagttt	ccaggctttg	1656
cagaagacct	tgtctcttta	gaaatgcccc	agaaattttc	cacacccctc	tgggtatcca	1716
tggagagcct	ggggccagat	atctggctca	tctctggcat	tgttctctct	ccctctcttc	1776
tgcctgtgtt	ggtggtggtt	gtggtggggg	aatgtggatg	ggggatgtcc	tggctgatgc	1836
ctgcacaaat	ttcctccacc	cctctctgct	tatcgtccct	gttttgaggg	ctatgaattg	1896
agttcttgtt	tccctgtctc	tctctagctc	tgggaccttc	ctgaacttgg	gacctatcac	1956
tccctctctc	tctctctctc	tctctctctc	tctctctctc	tctctctctc	tctctctctc	2016

```
<210> 14
<211> 270
<212> PRT
<213> Homo sapiens
```

• • • • •



Ala Arg His Arg Pro Arg Leu Ile Asp Trp Asp Ser Val Asp Asn His
65 70 75 80 85 90 95

Pho 0121 Lou 049 Phx 041 Dca 044 Hls 043 Wg 040 Sfo 011 Oly 009 Den 014 Hls 001

Gln Glu Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg
100 105 110

Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe
115 120 125

Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr
130 135 140

Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val
145 150 155 160

Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr
165 170 175

Val Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys
180 185 190

Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile
195 200 215

Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala
210 215 220

Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys
225 230 235 240

Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp
245 250 255

Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Thr
260 265 270

```
<211> 15
<212> 1247
<213> DNA
<214> Rattus sp.
```

2208
2212 2213
2216 2217 2218

141
Cys Gly His Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro
41 41
145
Ala Ser Leu Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val
10 55 60
149
gag gat gag ttt gaa tta tcc aag ggg tgt cac cga cat gag ggc ctg
Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
65 70 75 80
289
gaa caa ctc cag gaa cag acc aag ttc aca cgc aga gag ctg cag gtc
Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
85 90 95
337
ctg tac cga ggc ttc aag aac gaa tgc ccc agt ggg att gtc aac gag
Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
100 105 110
385
gag aac ttc aag cag att tat tct cag ttc ttt ccc caa gga gac tcc
Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser
115 120 125
433
agc aac tat gct act ttt ctc ttc aat gcc ttt gag acc aac cac gat
Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
130 135 140
481
ggc tct gtc agt ttt gag gac ttt gtg gct ggt ttg tgg gtg att ctt
Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
145 150 155 160
529
cgg ggg acc ata gat gat aga ctg agc tgg gct ttc aac tta tat gac
Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp
165 170 175
577
ctc aac aag gac ggc tgt atc aca aag gag gaa atg ctt gac att atg
Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met
180 185 190
625
gag ttc atc tat gac atg atg gac aag tac aca tac cct gct ctg gaa
Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg
195 200 205
673
gag gag gcc cca aga gaa cac gtg gag agc ttc ttc cag aag atg gac
Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp
210 215 220
721
agg caa aag gac ggc ggg ggg acc atc gag gaa ttc atc gac tct tct
Arg Asn Lys Arg Glu Met Met Met Met Met Met Met Met Met Met Met

TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT
 TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT
 TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT 1042
 TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT 1062
 TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT 1122
 TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT 1182
 TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT 1242
 TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT TTTTCTCT 1247

<210> 16
 <211> 257
 <212> PRT
 <213> Rattus sp.

<400> 16
 Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly
 1 5 10 15
 Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys
 20 25 30
 Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro
 35 40 45
 Ala Ser Leu Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val
 50 55 60
 Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
 65 70 75 80
 Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
 85 90 95
 Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
 100 105 110
 Glu Asn Phe Lys Gln Ile Thr Ser Gln Phe Ile Phe Ile Gly Asp Ser
 115 120 125
 Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
 130 135 140
 Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
 145 150 155
 Leu Asn Lys Arg Arg Tyr Ile Thr Lys Glu Glu Met Ile Arg Ile Met
 160 165 170

His His Ala Thr Arg Ala His Val Thr Ser Ile Ile Gln Lys Met Arg
 211 215 219
 Arg Asn Lys Asp Gly Val Val Thr Ile Gln Glu Phe Ile Glu Ser Cys
 223 230 235 240
 Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val
 245 250 255

Ile

<210> 17
 <211> 2343
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (131)..(990)

<400> 17
 cgggactctg aggtgggccc taaaatccag cgtccccag agaaaagcct tgcagcccc 60
 tactccggc cccagcccc agcaggctgc tggcggcca gggggcactg tgtgagcgcc 120
 ctatccggc caccgggcg cccctccac ggcccaggcg ggagcggggc gccggggggc 180
 atg cgg ggc caa ggc cga aag gag agt ttg tcc gaa tcc cga gat ttg 228
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
 1 5 10 15
 gac ggc tcc tat gac cag ctt acg ggc cac cct cca ggg ccc agt aaa 276
 Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
 20 25 30
 aaa gcc ctg aag cag cgt ttc ctc aag ctg ctg ccg tgc tgc ggg ccc 324
 Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 aa ggc cgc ccc tca gtc agt caa ala tta gtc ggc cca cca cca ctc 372
 Gln Ala Leu Pro Ser Val Ser Gln Thr Leu Ala Ala Phe Ala Ser Leu
 50 55 60
 cgc ccc cac aga ccc cgc ccg ctg gac cca gac agc gtg gag gat gag 420
 Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val Glu Asp Glu
 65 70 75 80
 ttc gaa ata taa acg ggc tgc cag cgc ctt gag gtc ctg caa caa ctc 468
 Phe Glu Thr Ala Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr

His Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr
 1 11

His Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr

612
 Lys Glu Ile Tyr Ser Gln Ile Phe Ile Gln Gly Asp Ser Ser Asn Tyr
 145 150 155

660
 Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val
 145 150 155 160

708
 Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr
 165 170 175

756
 Ile Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys
 180 185 190

804
 Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile
 195 200 205

852
 Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala
 210 215 220

900
 Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys
 225 230 235 240

948
 Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp
 245 250 255

990
 Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 260 265 270

tagctcccca gggagagggg ttagtgtgtc ccagggtaac catgctgtag cctagttcca 1050
 ggcaaaacta accctctctt cccgggggtt gtatctatc tacctgtacc ctgggtgtgt 1110
 tagggattca acatctgtgc ccttcagttg ttaggtctt ttagtaact gtaggagaa 1170
 ttaaatctaa ctcttcttgg ggtctcttgg ggtgtgtg tttctaac ctgaagacta 1230
 tcaccccttt ctgactgat acccagttgt gaggtaccc ctggtgttgg gaacgaccaa 1290
 agtggttctc tgcctcccca gccactctc gagacacaa ctgagaggga atattctctg 1350
 ctatgtgtgt tttctctatc ctgacggag atttctctc taagactcc tttctataga 1410

[illegible]

```

0210. 18
0211. 270
0212. PRT
0213. Mus musculus

```

```

R400: 18
Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
  1              5              10              15

Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
      20              25              30

Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
      35              40              45

Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro Ala Ser Leu
      50              55              60

Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val Glu Asp Glu
      65              70              75              80

Phe Glu Leu Ser Thr Val Cys His Arg Phe Glu Gly Leu Glu Gln Leu
      85              90              95

Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg
      100              105              110

Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe
      115              120              125              130

Arg Leu Ile Leu Ile Arg Ala Ile Arg Leu Asn His Arg Arg Pro Thr
      135              140              145              150

```

100							1							100						
116	Arg	Asp	Arg	Leu	Asn	Thr	Ala	116	Asn	Leu	Tyr	Asp	Leu	Asn	Lys					
140							140							140						
Asp	Gly	Tyr	116	Thr	Lys	Glu	Glu	Met	Leu	Asp	116	Met	Lys	Ser	Ile					
190							190							205						
Tyr	Asp	Met	Met	Gly	Lys	Tyr	Thr	Tyr	Pro	Ala	Leu	Arg	Glu	Glu	Ala					
210							215							220						
Pro	Arg	Glu	His	Val	Glu	Ser	Phe	Phe	Gln	Lys	Met	Asp	Arg	Asn	Lys					
225							230							235						
Asp	Gly	Val	Val	Thr	Ile	Glu	Glu	Phe	116	Glu	Ser	Cys	Gln	Gln	Asp					
245							250							255						
Glu	Asn	Ile	Met	Arg	Ser	Met	Gln	Leu	Phe	Asp	Asn	Val	Ile							
260							265							270						

```

0210 · 19
0211 · 1955
0212 · DNA
0213 · Homo sapiens

```

0220 .
 0221 . CDS
 0222 . (207) .. (962)

```

<400> 10
ctcacctgct gctagtggt cctctctctg ctccaggacc tccgggtaga cctcagaccc 60
cgggcacatt ccagactca gctcagccc ggacttccc agccccgaca gcacagtagg 120
cggccagggg ggcctgtgt agcgcctat cccggccacc cgggcacccc tcccacggcc 180
cgggggggag cgggggcgcg ggggcc atg cgg ggc cag ggc cgc aag gag agt 233
          Met Arg Gly Gln Gly Arg Lys Glu Ser
                1                5

```

ttg tgg gat tgg gga gaa ctg gaa gga tgg tac gaa gag ctg aag gga 231
 Leu Val Asp Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Gly
 10 15 20 25

His Pro Pro Gly Pro Thr Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys

etg etg ccc tgc tgc ggg ccc caa gcc etg ccc tca gtc agt gaa aac 377
 Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Gln Asn
 45 50 55

[illegible]

gag tcc agc acc tat gcc acg ttt ctg ctg aat gcc ttt gag acc aac 617
 Asp Ser Ser Thr Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn
 125 130 135

cat gat ggc tgg gtc agt ttt gag gac ttt gtg gct gat ttg tcc gtg 665
His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val
140 145 150

att ctt egg gga act gta gat gac agg ctt nat tgg gca ttc aac ctg 713
Ile Leu Arg Gly Thr Val Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu
155 160 165

tat gac ctt aac aag gac gcc tgc atc acc aag gag gaa atg ctt gac 761
Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp
170 175 180 185

atc atg aag tcc atc tat gac atg atg ggc aag tac aag tac cct gca 809
 Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala
 130 195 200

ctc cgg gag gag gcc cca agg gaa cac gtg gag agc ttc ttc cag aag 857
Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys
205 210 215

atg gac aga aac aag gat ggt gtg gtg acc att gag gaa tta att gag 905
Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu
220 225 230

tct tgt aag gat gag aac atc atg agg tcc atg cag ctc ttt gac 953
Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp
235 240 245

dat die ate tagenodag gemaakgt vertutten gemaakgt 1990
 Ast. Val. ile
 , 50

arjst etaa aragloag gaggaceta coiterett ocaagleta tectate et 1062

acgcctccct gggggctaga gggatccaag agcttgggga ttcagtagtc caatctctg 1122

jalet jaggg gggcagagag tgggcagagt gcatctcggy gqgtgtttrr aactcccaac 1182

* χ^2 -test; ** $p < 0.01$; *** $p < 0.001$.

aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 144
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 148
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 152
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 156
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 160
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 164
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 168
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 172
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 176
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 180
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 184
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 188
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 192
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 196
 aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt aaatggtt 200

<210> 20
 <211> 252
 <212> PRT
 <213> Homo sapiens

<400> 20
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu
 1 5 10 15
 Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Thr Lys
 20 25 30
 Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Asp Asp Glu Phe Glu
 50 55 60
 Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
 65 70 75 80
 Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg Gly Phe
 85 90 95
 Lys Asn Gln Cys Pro Ser Gly Ile Val Asn Gln Gln Asn Phe Lys Gln
 100 105 110
 Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
 115 120 125
 Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 130 135 140
 Tyr Arg Lys Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr
 145 150 155 160 165 170 175 180 185 190 195 200
 Tyr Ile Thr Lys Gln Gln Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
 205 210 215 220 225 230 235 240 245 250

Ser Met Gly Lys Tyr Thr Lys Phe Ala Leu Arg Ala Glu Ala Ile Arg
 10 20 30 40 50 60 70 80 90 100

His His Val Thr Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
 110 120 130 140 150 160 170 180 190 200

Val Val Thr Ile Glu Glu Phe Ile Ala Ser Lys Gln Lys Asp Gln Asn
 210 220 230 240 250 260 270 280 290 300

Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 310 320 330 340 350 360 370 380 390 400

<210> 21

<211> 2300

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> 214)..(969)

<400> 21

ctcatttgct gcccaagget cctgctcctg cccaggact ctgaggtggg ccctaaaacc 60

cagcgtcttc taaagaaaag ccttgccagc cctactccc ggcccccaac ccagcaggt 120

cgtgcacccg ccagggggcg ctgtgtgagc gccctattct ggccaccggg cgcacctctc 180

caaggccag gcgggagcgg ggccgcgggg gcc atg cgg gcc caa gcc aga aag 234
 Met Arg Gly Gln Gly Arg Lys
 1 5

gag agt ttg tcc gaa tcc cga gat ctg gac gcc tcc tat gac cag ctt 282
 Glu Ser Leu Ser Glu Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu
 10 15 20

acg gcc cac cct cca ggg ccc agt aaa aaa gcc ctg aag cag cgt ttc 330
 Thr Gly His Pro Pro Gly Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe
 25 30 35

ctc aag ctg ctg ccg tgc tgc ggg ccc caa gcc ctg ccc tca gtc agt 378
 Leu Lys Leu Leu Pro Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser
 40 45 50 55

gaa aac aac gaa aac aac aac ttc aac ttc ttc arg gtc tgc cag cga 420
 Glu Asn Ser Val Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg
 60 65 70

cct gag gcc ctg gaa caa ctc cag gaa cag acc aag ttc aca gcc aca 474
 Pro Glu Gly Leu Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg
 85 90 95

ctc aac aac aac aac aac aac aac aac aac aac aac aac aac aac aac aac
 100 110 120 130 140 150 160 170 180 190 200

[illegible]

[illegible]

```
<210> 12
<211> 152
<212> FRT
<213> Rattus sp.
```

Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Glu Ser Arg Asp Leu
 1 5 10 15
 Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
 20 25 30
 Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
 35 40 45
 Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Glu Asp Glu Phe Glu
 50 55 60
 Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
 65 70 75 80
 Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe
 85 90 95
 Lys Asn Gln Cys Pro Ser Gly Ile Val Asn Gln Gln Asn Ile Lys Gln
 100 105 110
 Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr Ala Thr
 115 120 125
 Phe Leu Phe Asn Ala Ile Asp Thr Asn His Asp Gly Ser Val Ser Phe
 130 135 140
 Asp Asn Leu Ser Thr Ala Ile Asn Leu Tyr Asp Leu Asn Tyr Asn Gly
 145 150 155 160

8411-14
 8411-15
 8411-16T
 8411- Ham. sapiens

8400-14
 Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu
 1 5 10 15
 Asp Gly Ser Tyr Asp Gln Leu Thr Asp Ser Val Asp Asp Glu Phe Glu
 20 25 30
 Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
 35 40 45
 Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg Gly Phe
 50 55 60
 Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
 65 70 75 80
 Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
 85 90 95
 Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 100 105 110
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
 115 120 125
 Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
 130 135 140
 Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
 145 150 155 160
 Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
 165 170 175
 Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
 180 185 190
 Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn
 195 200 205
 Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 210 215 220

8410-25
 8411-212

8411-213
 8411-214

.....
.....

.....
Met Arg Gly Ser Gly Arg Lys His Ser Leu Ser Asp Ser
1 5 11

aga gac ctg gac gga tcc tac gac cag ctc acg gac agc gtg gag gat 219
Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu Thr Asp Ser Val Glu Asp
15 20 25

gaa ttt gaa ttg tcc acc gtg tgt cac cgg cct gag ggt ctg gag cag 267
Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln
30 35 40 45

ctg cag gag caa acc aaa ttc acg cgc aag gag ttg cag gtc ctg tac 315
Leu Gln Glu Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr
50 55 60

cgg ggc ttc aag aac gaa tgt ccg agc gga att gtc aat gag gag aac 363
Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn
65 70 75

ttc aag caa att tac tcc cag ttc ttt cct caa gga gac tcc agc acc 411
Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr
80 85 90

tat gcc act ttt ctc ttc aat gcc ttt gac acc aac cat gat ggc tgg 459
Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser
95 100 105

gtc agt ttt gag gac ttt gtg gct ggt ttg tcc gtg att ctt cgg gga 507
Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly
110 115 120 125

act gta gat gac agg ctt aat tgg gcc ttc aac ttg tat gac ctc aac 555
Thr Val Asp Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn
130 135 140

aag gac ggc tgc atc acc aac cag caa atg ttc cag acc atg aag tcc 603
Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser
145 150 155

atc tat cag ttc ttc ttc aat tat aat tat ttc ttc ttc gag gag gag 651
Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu
160 165 170

gcc cca agg gaa cat gtg gag aac ttc ttc cag aag atg gac aga aac 699
Ala Pro Arg Glu His Val Glu Asn Phe Phe Gln Lys Met Asp Arg Asn
175 180 185

.....
Asp His Asn Ile Met Arg Ser Met Gln Leu Ile Arg Asn Val Ile
211 217

```
<210> 26
<211> 222
<212> ERI
<213> DIRECTOR
```

Leu Ser Thr Val Tyr His Asn His Ser Gly Leu Ser Gln Ser Gln Ala
 5 10 15 20 25 30 35 40 45 50 55 60
 Val Thr Lys Ile Thr Arg Lys His Leu Gln Val Leu Tyr Arg Gly Ser
 65 70 75 80 85 90 95
 Lys Asn Gln Cys Pro Ser Gly Ile Val Asn Gln Gln Asn Phe Lys Gln
 100 105 110 115 120 125 130 135 140
 Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
 145 150 155 160 165 170 175 180 185 190
 Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 195 200 205 210 215 220 225 230 235 240
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
 245 250 255 260 265 270 275 280 285 290
 Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
 295 300 305 310 315 320 325 330 335 340
 Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
 345 350 355 360 365 370 375 380 385 390
 Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
 395 400 405 410 415 420 425 430 435 440
 Glu His Val Glu Asn Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
 445 450 455 460 465 470 475 480 485 490
 Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn
 495 500 505 510 515 520 525 530 535 540
 Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
 545 550 555 560 565 570 575 580 585 590

<210> 27
 <211> 2057
 <212> DNA
 <213> Simian sp.

<220>
 <221> CDS
 <222> (200-111) (400-111)

<400> 27
 tgcctgcacaa ggcctcctgct cctgcctccag gaactctgagg tgggcctcaa aacccagagc 60
 tctctaaaga aaagccttgc cagccctctac tccgggcctc caactccagc aggtcctgtr 120
 ggcgcagggg ggcctctgct gagcgcctca ttctgcctac cccgggcctc ctcctccctc 180

<410> 27
 Leu Ser Thr Val Tyr His Asn His Ser Gly Leu Ser Gln Ser Gln Ala
 5 10 15 20 25 30 35 40 45 50 55 60

37
 His Pro Leu Gly Leu Ser Lys Lys Ala Leu Lys Val Asn Leu Lys
 45 50 55

378
 Leu Leu Val Cys Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Glu Asn
 45 50 55

426
 agc gta gag gat gag ttt gaa tta tcc acg gtg tgt cac cga cct gag
 Ser Val Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu
 60 65 70

474
 ggc ctg gaa caa ctc cag gaa cag acc aag ttc aca cgc aga gag ctg
 Gly Leu Glu Gln Leu Gln Gln Gln Thr Lys Phe Thr Arg Arg Glu Leu
 75 80 85

522
 cag gtc ctg tac cga ggc ttc aag aac gaa tgc ccc agt ggg att gtc
 Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val
 90 95 100 105

570
 aac gag gag aac ttc aag cag att tat tct cag ttc ttt ccc caa gga
 Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly
 110 115 120

618
 gac tcc agc aac tat gct act ttt ctc ttc aat gcc ttt gac acc aac
 Asp Ser Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn
 125 130 135

666
 cac gat ggc tct gtc agt ttt gag gac ttt gtg gct ggt ttg tgg gtg
 His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val
 140 145 150

714
 att ctt cgg ggg acc ata gat gat aga ctg agc tgg gct ttc aac tta
 Ile Leu Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu
 155 160 165

762
 tat gac ctc aac aag gac ggc tgt atc aca aag gag gaa atg ctt gac
 Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp
 170 175 180 185

810
 att atg aag tcc atc tat gac atg atg ggc aag tac aca tac cct gcc
 Ile Met Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala
 190 195 200

858
 cta ggt gat agt tta cca aca caa cag gty gta agt tta tta cag aag
 Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys
 205 210 215

906
 atg gac agg aac aag gac ggc gtg gtg acc atc gag gaa ttc atc gag
 Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu
 220 225 230

954
 cta ggt gat agt tta cca aca caa cag gty gta agt tta tta cag aag
 Leu Arg Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys
 205 210 215

```
<210> 25
<211> 252
<212> PRT
<213> Simian sp.
```

Lys Asn Glu Lys Trp Ser Gly Ile Val Asn Glu Val Asn Ile Lys Val
100 105 110

Ile Tyr Ser Glu Phe Ile Trp Glu Gly Asp Ser Ser Asn Tyr Ala Thr
115 120 125

Phe Leu Ile Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
130 135 140

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp
145 150 155 160

Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
165 170 175

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
180 185 190

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
195 200 205

Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
210 215 220

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp Glu Asn
225 230 235 240

Ile Met Arg Ser Met Gln Leu Ser Pro Leu Leu Asn
245 250

<110> 29

<111> 1904

<112> DNA

<113> Rattus sp.

<120>

<121> CDS

<122> (1)..(675)

<400> 29

arg aac aac tgc cct cgc agg tgc agg aac aac tgg ggg cac tca ggt 48
Met Asn His Cys Pro Arg Arg Cys Arg Ser Pro Leu Gly Gln Ala Ala
1 5 10 15

gaa ttt gaa ttt tgg ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 80
Arg Ser Leu Tyr Gln Leu Val Thr Gly Ser Leu Ser Pro Asp Ser Val
20 25 30

gag gat gag ttt gaa tta tcc aac gtg tct cag cga cct gag cga ctg 144
Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
35 40 45

gaa ttt gaa ttt tgg ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 160
Leu Tyr Arg Gly Ile Lys Asn Glu Tyr Pro Ser Gly Ile Val Asn Glu
45 50 55

[illegible]

0210 - 30
 0211 - 225
 0212 - FET
 0213 - Rattus sp.

```

0400 - 30
Met Asn His Cys Pro Arg Arg Cys Arg Ser Pro Leu Gly Gln Ala Ala
  1          5          10          15

Arg Ser Leu Tyr Gln Leu Val Thr Gly Ser Leu Ser Pro Asp Ser Val
          20          25          30

Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
          35          40          45

Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
          50          55          60

Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
  65          70          75          80

Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser
          85          90          95

Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
          100          105          110

Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
          115          120          125

Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp
          130          135          140

Lys Ser Ile Tyr Arg Met Met Gly Tyr Tyr Thr Tyr Ile Asn Leu Ala
          145          150          155

```

Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Ile Ile Glu Ser Lys
175 201

Gln Glu Asp Glu Asn Ile Met Arg Ser Met Gln Leu Ile Asp Asn Val
210 215 220

Ile
225

<210> 31
<211> 2841
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(768)

<400> 31
atg cag ccg gct aag gaa gtg aca aag ggc tcg gac ggc agc ctc ctg 48
Met Gln Pro Ala Lys Glu Val Thr Lys Ala Ser Asp Gly Ser Leu Leu
1 5 10 15
ggg gac ctc ggg cac aca cca ctt agc aag aag gag ggt atc aag tgg 96
Gly Asp Leu Gly His Thr Pro Leu Ser Lys Lys Glu Gly Ile Lys Trp
20 25 30
cag agg ccg agg ctc agc cgc cag gct ttg atg aga tgc tgc ctg gtc 144
Gln Arg Pro Arg Leu Ser Arg Gln Ala Leu Met Arg Cys Cys Leu Val
35 40 45
aag tgg atc ctg tcc agc aca gcc cca cag ggc tca gat agc agc gac 192
Lys Trp Ile Leu Ser Ser Thr Ala Pro Gln Gly Ser Asp Ser Ser Asp
50 55 60
agt gag ctg gag ctg tcc acg gtg cgc cac cag cca gag ggg ctg gac 240
Ser Glu Leu Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp
65 70 75 80
cag ctg cag gac cag acc aag ttc acc aag aag gag ctg cag tct ctc 288
Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu
85 90 95
tac agg ggc ttt aag aat gag tgt ccc aag ggc ctg gtg gac gaa gac 336
Tyr Arg Gly Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp
100 105 110
atc ttc aaa ctc att tac gag caa ttc ttc cct cag aga gat ggc acc 384
Thr Phe Lys Leu Ile Tyr Ala Gln Phe Phe Pro Gln Gly Asp Ala Thr
115 120 125 130 135
gaa att att att att att att att att att att att att att att att 432
Ala Ile His Phe Glu Asn Phe Thr Thr Thr Thr Thr Thr Thr Thr Thr
140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

[illegible]

Asn Lys Asp Gly Tyr His Thr Lys Glu Glu Met Leu Ala Phe Met Lys
180 190 200

ttc atc tat gac atg atg ggc cgc cac acc tac ccc atc ctg cgg gag 624
 Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
 195 200 205

gac gag cag gag gag cac gtg gag agg ttc ttc gag aaa atg gac cgg 672
Asp Ala Pro Ala Glu His Val Glu Arg Phe Phe Glu Lys Met Asp Arg
210 215 220

aac cag gat ggg gta gtg acc att gaa gag ttc ctg gag gcc tgt cag 720
Asn Gln Asp Gly Val Val Thr Ile Glu Glu Phe Leu Glu Ala Cys Gln
225 230 235 240

aag gat gag aac atc atg agc tcc atg cag ctg ttt gag aat gtc atc 768
Lys Asp Glu Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
245 250 255

taggacacgt ccaaaggagt gcatggccac agccacctcc accccaaga aacctccatc 828

ctgccaggag cagcctccaa gaaactttta aaaaatagat ttgcacaaaag tgaacacgatt 888

gctacacaca cacacacaca cacacacaca cacacacaca cacagccatt catctgggct 948

ggcagagggg acagaggtca gggagggggt gagtctgggt aggggcccag tccaggagcc 1008

ccagccagcc ctccccagcc cagccagccg aggcgcgcgc tgggtgagtg gctcacagag 1068

caqgtctgca ggcacaccagc tgetggatgt caccaagaac gggctcgagt gccctgcag 1128

gggagggtcc aatctccggt gtgagccac ctgctccgt tctccattct gctttcttgc 1188

cacacagtgg gccggcccca ggtccctctg gtctctccc cgtagccact ctctgccac 1248

tacatatgat tctagaaagc cccctacctc aggaacccan aggaaccayc t tgggggca 1308

000000000 000000000 000000000 000000000 000000000 000000000 000000000

[illegible]

gggcaagcct gactggttag aggcactgag gccccattct cctccatgag caqaaaggcg 1488

gggatttca agtttanga ttgggtctg ttggagaatc ttgggggcat ctctggcagc 1646

[illegible]

1. *Journal of the American Medical Association*, 1997; 277: 1033-1036.



Thr Tyr Ala His Thr Leu Phe Asn Ala Thr Asp Ala Asp Gly Asn Gly
180 185 190

Ala Thr His Thr Glu Asp Phe Val Val Gly Leu Ser Thr Leu Leu Arg
145 150 155 160

Gly Thr Val His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile
165 170 175

Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys
180 185 190

Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
195 200 205

Asp Ala Pro Ala Glu His Val Glu Arg Phe Phe Glu Lys Met Asp Arg
210 215 220

Asn Glr. Asp Gly Val Val Thr Ile Glu Glu Phe Leu Glu Ala Cys Gln
235 230 235 240

Lys Asp Glu Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
245 250 255

<P10> 33
<P11> 442
<P12> DNA
<P13> Rattus sp.

<200:
<210: CDS
<222: (1)..(327)

<400> 33
ttt gag gac ttt gtg qtt ggg ctc tcc atc ctg ott cga ggg acc gtc 48
Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg Gly Thr Val
1 5 10 15

His Glr Lys Ser Lys Thr Ala Phe Asn Leu Tyr Asp Ile Asn Lys Arg

20 25 30

ggt tac atc acc aaa gag gag atg ctg gcc atc atg aag tcc atc tac 144
Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
35 40 45

Arg Val Val Ile Ile Asp Ala Ile Ile Val Thr Tyr Val Lys Arg Val
1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100

Asn Ile Met Ser Ser Met Val Leu Ile Ala Asn Val Ile
105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200

aggadgggag catggggggc catgggttct caaaccagag aggtctaat catgacagga 397

gaagactata agagaaacat ttttctaata tatttgaaa aagtg 442

<210> 34
<211> 109
<212> PRT
<213> Rattus sp.

<400> 34
Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg Gly Thr Val
1 5 10 15

His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp
20 25 30

Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
35 40 45

Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu Asp Ala Pro
50 55 60

Leu Glu His Val Glu Arg Phe Phe Gln Lys Met Asp Arg Asn Gln Asp
65 70 75 80

Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln Lys Asp Glu
85 90 95

Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
100 105

<210> 35
<211> 2644
<212> DNA
<213> Mus musculus

<210>
<221> CDS
<222> (49)..(816)

<400> 35
gggtctgaa aggggaga taatgagc tttttat caggag ag ag ag
Met Gln Arg

gggtctgaa aggggaga taatgagc tttttat caggag ag ag ag
Met Gln Arg

agg tta att att att att att att att att att att att att att att att att 441
Arg Ile Thr Arg Gln Ala Leu Met Asn Tyr Tyr Leu Ile Lys Thr Ile
40 45 45

agg tta att att att att att att att att att att att att att att att att 244
Leu Ser Ser Ala Ala Pro Gln Gly Ser Asp Ser Ser Asp Ser Glu Leu
55 60 65

gag tta tcc aag gtg cgc cat cag cca gag ggc ttg gac cag cta caa 297
Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp Gln Leu Gln
70 75 80

gct cag acc aag ttc acc aag aag gag ctg cag tcc ctt tac cga ggc 345
Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu Tyr Arg Gly
85 90 95

ttc aag aat gag tgt ccc aca ggc ctg gtg gat gaa gac acc ttc aaa 393
Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp Thr Phe Lys
100 105 110 115

ctc att tat tcc cag ttc ttc cct cag gga gat gcc acc acc tat gca 441
Leu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ala Thr Thr Tyr Ala
120 125 130

cac ttc ctc ttc aat gcc ttt gat gct gat ggg aac ggg gcc atc cac 489
His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly Ala Ile His
135 140 145

ttt gag gac ttt gtg gtt ggg ctc tcc atc ctg ctt cga ggg aag gtc 537
Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg Gly Thr Val
150 155 160

cat gag aag ctc aag tgg gcc ttc aat ctc tat gac att aac aag gat 585
His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp
165 170 175

ggt tgc atc acc aag gag gag atg ctg gcc atc atg aag tcc atc tac 633
Gly Cys Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
180 185 190 195

gac atg atg ggc cgc cac acc tac ccc atc ctg cgg gag gat gca ccc 681
Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu Asp Ala Pro
200 205 210

ctc att att att att att att att att att att att att att att att att 721
Leu Glu His Val Glu Arg Phe Phe Gln Lys Met Asp Arg Asn Gln Asp
215 220 225

gga ctg gtg acc att gat gaa ttt ctg gag act tgt cag aag gat gag 777
Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln Lys Asp Glu
230 235 240

|||||

|||||

taataatata taataatata taataatata taataatata taataatata 1206
taataatata taataatata taataatata taataatata taataatata 1207
taataatata taataatata taataatata taataatata taataatata 1208
taataatata taataatata taataatata taataatata taataatata 1209
taataatata taataatata taataatata taataatata taataatata 1210
ggagatcaaa caactcaatg ccatgggacc catgcctta ggaagctccc agaaactca 1246
aggggacaaa gaggggagag gtatatagga agaaatggtt ttggaagctg ggcttgacag 1306
cttatgtcaa tgatcaatg gggtcctgga acccgagtga caggctacat actatgcctg 1366
gagcttagat agtgaggggg cattgggacta agacctcctg taagagtggg gcaggattga 1426
ggtttttggg gaaactgagg aaacaatttg tccataccac tgggtgaaga ctgctggcca 1486
gtgggaatgt ggctgggtgga gatttcccaa cttccagcac caggatgggc tctccaaggt 1546
cctctttgat tccctgggga gatcaatggt ctcatagact gacaaccagg gaactgggct 1606
gaaatgggag gtctggtagg gggaatcccc ctcttttctc ctggccactt gccaccaggt 1666
tcttaacac agtggatcgg ccacacctct gtggctgccc ttgaacagac tcatcccgac 1726
caagacaaaa aagcacaaa ccttagcagc tcaggccaag ccacaaaggg aaggcctggg 1786
tccctgcagc cctgattcag tggccgagga agacgctcag acatccatcc tgtacctcgg 1846
agccttgggg gtctcaccag ccttccccag ccagctcgc caacattcta aagcacaaa 1906
ctgaggatto tcttgcctg ggctgcgccc tggggattga aggcactgt taacctaa 1966
ctggagctag cctgagggg tggggacctg tgaccaggca acaggtcagc agacccctag 2026
gaggagagag agctgttctt gctcccccag gctcgcacca gaaggaaacag tgtcccaaga 2086
agcatgtttt ctggaggaac atccccacaa aagtacatto catcatctga agcccggtct 2146
ctgctcaggc ctgctctga aagtcacagt gtgttcccca gaaggccagc cccaagataa 2206
ggagctctt taaggaagg aaggggtgac caaacctta taccacgtt gaaacccct 2266
tgagggtt taatgacac atctcctctc tgaaggggc ctctctta taatctata 2326
gaccacagct tctccctggc ccagggaacc ctgtccccc agcttgacta tctccataga 2386
ggtccctgtt ttgtgaaaag ccaaggccac gggaaaaggc caccactcta acctgtctga 2446
taattatata ttgggtata cgaacacat ggagggtct gtaatttg taatgata 2506
taattatata taatgata taatgata taatgata taatgata

01/10/1981

01/10/1981 MNI-070CP4

04/01/86

Ser Ala Arg Thr Lys Gln Ala Val Lys Ala Ser Asp Gly Asn Leu Leu
1 5 10 15

Gly Asp Pro Gly Arg Ile Pro Leu Ser Lys Arg Glu Ser Ile Lys Trp
20 25 30

Gln Arg Pro Arg Phe Thr Arg Gln Ala Leu Met Arg Cys Cys Leu Ile
35 40 45

Lys Trp Ile Leu Ser Ser Ala Ala Pro Gln Gly Ser Asp Ser Ser Asp
50 55 60

Ser Glu Leu Glu Leu Ser Thr Val Arg His Gln Pro Glu Gly Leu Asp
65 70 75 80

Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu
85 90 95

Tyr Arg Gly Phe Lys Asn Glu Cys Pro Thr Gly Leu Val Asp Glu Asp
100 105 110

Thr Phe Lys Leu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ala Thr
115 120 125

Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly
130 135 140

Ala Ile His Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg
145 150 155 160

Gly Thr Val His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile
165 170 175

Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys
180 185 190

Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
195 200 205

Asp Ala Pro Leu Gln His Val Gln Arg Phe Phe Gln Lys Met Asp Arg
210 215 220

Asn Gln Asp Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln
225 230 235 240

Lys Asp Glu Asn Ile Met Asn Ser Met Gln Leu Phe Gln Asn Val Ile
245 250 255

01/10/1981

01/10/1981 MNI-070CP4

04/01/86

GenBank: D12111.1

Seq 1

Cloned At position 496, in myc min. gene

<400> 37

tac aag ggg gaa agc att tgg gct cag ctg gag gag ggc agc tct aca 48
His Glu Val Glu Ser Ile Ser Ala Gln Leu Glu Glu Ala Ser Ser Thr
1 5 10 15

ggc ggt ttc ctg tac gct cag aac agc acc aag cgc agc att aaa gag 96
Gly Gly Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser Ile Lys Glu
20 25 30

cgg ctg atg aag ctg ttg ccc tgc tca gct gcc aaa acg tgg tct cct 144
Arg Leu Met Lys Leu Leu Pro Cys Ser Ala Ala Lys Thr Ser Ser Pro
35 40 45

gct att caa aac agc gtg gaa gat gaa ctg gag atg gcc acc gtc agg 192
Ala Ile Gln Asn Ser Val Glu Asp Glu Leu Glu Met Ala Thr Val Arg
50 55 60

cat cgg ccc gaa gcc ctt gag ctt ctg gaa gcc cag agc aaa ttt acc 240
His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys Phe Thr
65 70 75 80

aag aaa gag ctt cag atc ctt tac aga gga ttt aag aac gta aga act 288
Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Val Arg Thr
85 90 95

ttc ttt ttg act tta cct tca cac aat tcc cag agg agc att gag aaa 336
Phe Phe Leu Thr Leu Pro Ser His Asn Ser Gln Arg Ser Ile Glu Lys
100 105 110

tgagaggaaa aggggggaaaa tatcccatc tatgagaagc cccatcatat gtatatttca 396

tactgatcct tcccagatag gaatataatc agtatctgtg gactttgaat ctctgtggca 456

cacccatgct ggcatactgt aattgcccat taaacaaana gtttttgaga aaaaaaaaaa 516

aaaaaaaaaa aaaaaa 531

<210> 38

<211> 116

<212> FRT

<213> Homo sapiens

<400> 38

His Glu Val Glu Ser Ile Ser Ala Gln Leu Glu Glu Ala Ser Ser Thr
1 5 10 15

Gly Gly Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser Ile Lys Glu

Ala Ile Gln Asn Ser Val Glu Asp Glu Leu Glu Met Ala Thr Val Arg
50 55 60

His Arg Pro Ala Ala Leu Ala Leu Leu Ala Ala Gln Ser Lys Phe Thr
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Lys Lys Ala Leu Ala Ile Leu Tyr Arg Gly Phe Lys Asn Val Arg Thr
21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40

Ile Phe Leu Thr Leu Pro Ser His Asn Ser Gln Arg Ser Ile Glu Lys
41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
100 105 110

<210> 39

<211> 2176

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(124)

<400> 39

t gaa agg ttc ttc gag aaa atg gac cgg aac cag gat ggg gta gtg acc 49
Glu Arg Phe Phe Glu Lys Met Asp Arg Asn Gln Asp Gly Val Val Thr
1 5 10 15

att gaa gag ttc ctg gag gcc tgt cag aag gat gag aac atc atg agc 97
Ile Glu Glu Phe Leu Glu Ala Cys Gln Lys Asp Glu Asn Ile Met Ser
20 25 30

tcc atg cag ctg ttt gag aat gtc atc taggacacgt ccaaaggagt 144
Ser Met Gln Leu Phe Glu Asn Val Ile
35 40

gcacggccac agccacctcc acccccaga aacctccatc ctgccaggag cagcctccaa 204

gaaactttta aaaaatagat ttgcaaaaag tgaacagatt gctacacaca cacacacaca 264

cacacacaca cacacacaca cacagccatt catctgggct ggcagagggg acagagtcca 324

gggaggggct gaggctggct aggggcagag tccaggagcc ccagccagcc ctcccaggc 384

cagcagggcg aggetgcctc tgggtgagtg gctgacagag caggctctga ggcacaccgc 444

tgttggttgt caccagaag gggctagat ggcctgag gtaggtcc aatctcggc 504

ggttctctct cgtctctct cgtctctct ggtctctct cgtctctct ggtctctct 564

ggctccctct ggtctctct cgtctctct ctctgcccac tacctatgct tetagaaagc 624

cctcaccctc aggcacccag agggaccagc tggggggcag gggggagagg gggtaatgga 684

ggttaagctt cagctctct cgtctctct cgtctctct cgtctctct cgtctctct 744

cgtctctct cgtctctct cgtctctct cgtctctct cgtctctct cgtctctct 804

ggtctctct cgtctctct cgtctctct cgtctctct cgtctctct cgtctctct 904

ggtctctct cgtctctct cgtctctct cgtctctct cgtctctct cgtctctct 964

```

1114
1124
1134
1204
1214
1224
1234
1244
1254
1264
1274
1284
1294
1304
1314
1324
1334
1344
1354
1364
1374
1384
1394
1404
1414
1424
1434
1444
1454
1464
1474
1484
1494
1504
1514
1524
1534
1544
1554
1564
1574
1584
1594
1604
1614
1624
1634
1644
1654
1664
1674
1684
1694
1704
1714
1724
1734
1744
1754
1764
1774
1784
1794
1804
1814
1824
1834
1844
1854
1864
1874
1884
1894
1904
1914
1924
1934
1944
1954
1964
1974
1984
1994
2004
2014
2024
2034
2044
2054
2064
2074
2084
2094
2104
2114
2124
2134
2144
2154
2164
2176

```

<210> 40

<211> 41

<212> PRT

<213> Homo sapiens

<400> 41

```

Glu Arg Phe Phe Glu Lys Met Asp Arg Asn Gln Asp Gly Val Val Thr
  1             5             10             15

```

```

Ile Glu Glu Phe Leu Glu Ala Cys Gln Lys Asp Glu Asn Ile Met Ser
  20             25             30

```

<214> PRT
 <215> Homo sapiens

<216> PRT
 <217> Homo sapiens

111 112 113 114 115 116 117 118 119 120 121 122 123 124 125
 Leu Arg Gln Gln Ala Pro Arg Glu His Val Gln Ser Phe Ile Gln Lys
 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125
 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140
 Met Asp Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu
 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140
 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155
 Ser Cys Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu Ser Pro
 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155
 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170
 Leu Leu Asn
 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170
 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185
 gtggtttctcc acctttctagt cccactctag aaaccacatt agacagaagg tctctgtcta 1053
 tgggtgcttcc cccatcccta atctcttaga tttctctcga gactcccttc tcagagaaca 1123
 cgtctctgccc atgtcccccag ctggcttctc agcctagcct ttgagggccc tgtggggagg 1183
 cgggggacaag aaagcagaaa agtcttggcc ccgagccagt ggtaggtccc taggaattgg 1243
 ctggagtggg ggcacagaaag cctgggcaga tgatgagagc ccagctgggc tgtcactgca 1303
 gggtccgggg cctacagccc tgggtcagca gagtatgagt tccagactt tccagaaggt 1363
 ccttagcaat gtcccagaaa ttcaccgtac aactctcagt gtcttaggag ggcccgggat 1423
 ccagatgtct ggttccatccc tgaatcctct cctctcttct tctctgtatg gtgggagtgg 1483
 tggccagggg aagatgagtg gtgtcccgga tgatgctgt caaggtccc cctccctccc 1543
 ggtgtttctc atgacagctg tttggttctc catgaacctt atctagatgt agaggcatgg 1603
 agtgagtcag ggatttcccg aacttgagtt ttaccacttc tcttagtggc tgccttaggg 1663
 gaatgggaag aaccacagtgt gggggcacc attagaattt ttgcacgggt cctcacaatg 1723
 ccttagggtc ccttagggta cccgtctcct ctggttagtc taccagaga tgcctctgag 1783
 ctctctctct ggttagggat ggttaggtct aggtccatct tcttaggtt agcaattg 1843
 catgtctgtg ctctcatta acaaacctgc ttgtctcttc ctgcgcctct tctcagtcag 1903
 ccagggctct aggggaaggg cctcccgctt ccccatccgt cagacatggt tgactgcttt 1963
 acatttggg cctctctctc tctttctat cttatgagat cagatctat aagacattg 2023

Met Arg Lys Val Lys Arg Lys Val Ser Leu Ser Val Ser Arg Arg Leu
1 10 19 28 37 46 55 64 73 82 91 100 109 118 127 136 145 154 163 172 181 190 199 208 217 226 235 244 253 262 271 280 289 298 307 316 325 334 343 352 361 370 379 388 397 406 415 424 433 442 451 460 469 478 487 496 505 514 523 532 541 550 559 568 577 586 595 604 613 622 631 640 649 658 667 676 685 694 703 712 721 730 739 748 757 766 775 784 793 802 811 820 829 838 847 856 865 874 883 892 901 910 919 928 937 946 955 964 973 982 991 1000

Asp Gly Ser Tyr Asp Val Leu Thr Lys His Trp Val Lys Lys Ser Lys
10 19 28 37 46 55 64 73 82 91 100 109 118 127 136 145 154 163 172 181 190 199 208 217 226 235 244 253 262 271 280 289 298 307 316 325 334 343 352 361 370 379 388 397 406 415 424 433 442 451 460 469 478 487 496 505 514 523 532 541 550 559 568 577 586 595 604 613 622 631 640 649 658 667 676 685 694 703 712 721 730 739 748 757 766 775 784 793 802 811 820 829 838 847 856 865 874 883 892 901 910 919 928 937 946 955 964 973 982 991 1000

Lys Ala Leu Lys Val Arg Phe Leu Lys Leu Leu Pro Cys Lys Gly Pro
35 44 53 62 71 80 89 98 107 116 125 134 143 152 161 170 179 188 197 206 215 224 233 242 251 260 269 278 287 296 305 314 323 332 341 350 359 368 377 386 395 404 413 422 431 440 449 458 467 476 485 494 503 512 521 530 539 548 557 566 575 584 593 602 611 620 629 638 647 656 665 674 683 692 701 710 719 728 737 746 755 764 773 782 791 800 809 818 827 836 845 854 863 872 881 890 899 908 917 926 935 944 953 962 971 980 989 998 1007

Gln Ala Leu Pro Ser Val Ser Glu Asn Ser Val Glu Asp Glu Phe Glu
50 59 68 77 86 95 104 113 122 131 140 149 158 167 176 185 194 203 212 221 230 239 248 257 266 275 284 293 302 311 320 329 338 347 356 365 374 383 392 401 410 419 428 437 446 455 464 473 482 491 500 509 518 527 536 545 554 563 572 581 590 600 609 618 627 636 645 654 663 672 681 690 699 708 717 726 735 744 753 762 771 780 789 798 807 816 825 834 843 852 861 870 879 888 897 906 915 924 933 942 951 960 969 978 987 996 1005

Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Gln Glu
65 74 83 92 101 110 119 128 137 146 155 164 173 182 191 200 209 218 227 236 245 254 263 272 281 290 299 308 317 326 335 344 353 362 371 380 389 398 407 416 425 434 443 452 461 470 479 488 497 506 515 524 533 542 551 560 569 578 587 596 605 614 623 632 641 650 659 668 677 686 695 704 713 722 731 740 749 758 767 776 785 794 803 812 821 830 839 848 857 866 875 884 893 902 911 920 929 938 947 956 965 974 983 992 1001

Gln Thr Lys Phe Thr Arg Arg Glu Leu Glu Val Leu Tyr Arg Gly Phe
80 89 98 107 116 125 134 143 152 161 170 179 188 197 206 215 224 233 242 251 260 269 278 287 296 305 314 323 332 341 350 359 368 377 386 395 404 413 422 431 440 449 458 467 476 485 494 503 512 521 530 539 548 557 566 575 584 593 602 611 620 629 638 647 656 665 674 683 692 701 710 719 728 737 746 755 764 773 782 791 800 809 818 827 836 845 854 863 872 881 890 899 908 917 926 935 944 953 962 971 980 989 998 1007

Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
100 109 118 127 136 145 154 163 172 181 190 200 209 218 227 236 245 254 263 272 281 290 300 309 318 327 336 345 354 363 372 381 390 400 409 418 427 436 445 454 463 472 481 490 500 509 518 527 536 545 554 563 572 581 590 600 609 618 627 636 645 654 663 672 681 690 700 709 718 727 736 745 754 763 772 781 790 800 809 818 827 836 845 854 863 872 881 890 899 908 917 926 935 944 953 962 971 980 989 998 1007

Ile Tyr Ser Glu Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr Ala Thr
115 124 133 142 151 160 169 178 187 196 205 214 223 232 241 250 259 268 277 286 295 304 313 322 331 340 349 358 367 376 385 394 403 412 421 430 439 448 457 466 475 484 493 502 511 520 529 538 547 556 565 574 583 592 601 610 619 628 637 646 655 664 673 682 691 700 709 718 727 736 745 754 763 772 781 790 800 809 818 827 836 845 854 863 872 881 890 899 908 917 926 935 944 953 962 971 980 989 998 1007

Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
130 139 148 157 166 175 184 193 202 211 220 229 238 247 256 265 274 283 292 301 310 319 328 337 346 355 364 373 382 391 400 409 418 427 436 445 454 463 472 481 490 500 509 518 527 536 545 554 563 572 581 590 600 609 618 627 636 645 654 663 672 681 690 700 709 718 727 736 745 754 763 772 781 790 800 809 818 827 836 845 854 863 872 881 890 899 908 917 926 935 944 953 962 971 980 989 998 1007

Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp
145 154 163 172 181 190 200 209 218 227 236 245 254 263 272 281 290 300 309 318 327 336 345 354 363 372 381 390 400 409 418 427 436 445 454 463 472 481 490 500 509 518 527 536 545 554 563 572 581 590 600 609 618 627 636 645 654 663 672 681 690 700 709 718 727 736 745 754 763 772 781 790 800 809 818 827 836 845 854 863 872 881 890 899 908 917 926 935 944 953 962 971 980 989 998 1007

Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
165 174 183 192 201 210 219 228 237 246 255 264 273 282 291 300 309 318 327 336 345 354 363 372 381 390 400 409 418 427 436 445 454 463 472 481 490 500 509 518 527 536 545 554 563 572 581 590 600 609 618 627 636 645 654 663 672 681 690 700 709 718 727 736 745 754 763 772 781 790 800 809 818 827 836 845 854 863 872 881 890 899 908 917 926 935 944 953 962 971 980 989 998 1007

Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
180 189 198 207 216 225 234 243 252 261 270 279 288 297 306 315 324 333 342 351 360 369 378 387 396 405 414 423 432 441 450 459 468 477 486 495 504 513 522 531 540 549 558 567 576 585 594 603 612 621 630 639 648 657 666 675 684 693 702 711 720 729 738 747 756 765 774 783 792 801 810 819 828 837 846 855 864 873 882 891 900 909 918 927 936 945 954 963 972 981 990 1000

Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
195 204 213 222 231 240 249 258 267 276 285 294 303 312 321 330 339 348 357 366 375 384 393 402 411 420 429 438 447 456 465 474 483 492 501 510 519 528 537 546 555 564 573 582 591 600 609 618 627 636 645 654 663 672 681 690 700 709 718 727 736 745 754 763 772 781 790 800 809 818 827 836 845 854 863 872 881 890 899 908 917 926 935 944 953 962 971 980 989 998 1007

Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
210 219 228 237 246 255 264 273 282 291 300 309 318 327 336 345 354 363 372 381 390 400 409 418 427 436 445 454 463 472 481 490 500 509 518 527 536 545 554 563 572 581 590 600 609 618 627 636 645 654 663 672 681 690 700 709 718 727 736 745 754 763 772 781 790 800 809 818 827 836 845 854 863 872 881 890 899 908 917 926 935 944 953 962 971 980 989 998 1007

Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp Glu Asn
225 234 243 252 261 270 279 288 297 306 315 324 333 342 351 360 369 378 387 396 405 414 423 432 441 450 459 468 477 486 495 504 513 522 531 540 549 558 567 576 585 594 603 612 621 630 639 648 657 666 675 684 693 702 711 720 729 738 747 756 765 774 783 792 801 810 819 828 837 846 855 864 873 882 891 900 909 918 927 936 945 954 963 972 981 990 1000

Ile Met Arg Ser Met Gln Leu Ser Trp Leu Leu Asn
245 254 263 272 281 290 300 309 318 327 336 345 354 363 372 381 390 400 409 418 427 436 445 454 463 472 481 490 500 509 518 527 536 545 554 563 572 581 590 600 609 618 627 636 645 654 663 672 681 690 700 709 718 727 736 745 754 763 772 781 790 800 809 818 827 836 845 854 863 872 881 890 899 908 917 926 935 944 953 962 971 980 989 998 1007

<210> 43

<211> 26

<212> PRT

1 1000

1 1000

1 1000

1 1000

100

U.S. Department of Justice
Federal Bureau of Investigation
Washington, D.C. 20535

1. *Chlorophyll a* (Chl *a*)

Phe His Met Met Met Met Met Met Met Met Asp Lys Asp Gly Asp Gly Met
 1 5 10 15

Xaa Xaa Xaa Xaa Glu Phe Xaa Xaa Xaa Xaa
20 25

4210. 44

5211 · 40

(212) DNA

4213. *Fattus* sp.

4400-44

taataacgaact cactataggg actggccatc ctgctctcag 40

(210) 45.

4211: 40

2.1.2. DNA

42130 Fattus sp.

44000 45

tttaaccctc actaaaggga cactactggt taagctcaag 40

4210 46

(211) 4C

3212 LINA

(213) Fattus sp.

4000 46

taatacgaact cactataggg cacctccctt ccggctgttc 40

<210> 47

(211) 40

21.1 DNA

015 - Rattus sp.

[illegible]

attaaacccctc actaaagqgga gaggcagcagc atgucaggggt 40

<210> . 48

622 2413

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains.

[illegible]

Figure 1 consists of two schematic diagrams. Diagram (a) is labeled 'Pretest' and shows a subject sitting at a table, looking at a screen. A camera is positioned above the screen. Diagram (b) is labeled 'Main experiment' and shows a subject sitting at a table, looking at a screen. A camera is positioned above the screen. A 'Start' button is on the table, and a 'Stop' button is on the wall.

[illegible]

ctg att cat ttg ctg gga ctg att gat ttt tgg gaa gac agc gtg gaa 387
Leu Leu His Leu Leu Gly Leu Ile Asp Phe Ser Glu Asp Ser Val Glu
30 35 40

ctt ctg gaa gcc cag agc aaa ttt acc aag aaa gag ctt cag atc ctt 483
Leu Leu Glu Ala Gln Ser Lys Phe Thr Lys Lys Glu Leu Gln Ile Leu
60 65 70

and ttc aaa gag att tac tgg cag ttc ttt cca cag gga gac tct aca 579
 Thr Phe Lys Glu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Thr
 90 95 100 105

get gtg agt ttc gag gat ttc atc aaa ggt ctt tcc att ttg ctg cgg 675
 Ala Val Ser Phe Glu Asp Phe Ile Lys Gly Leu Ser Ile Leu Leu Arg
 125 130 135

aat aaa gat ggc tac atc aac aaa gag gaa atg ctt gat ata atg aaa 771
Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys
155 160 165

Ala Ile Tyr Asp Met Met Gly Lys Cys Thr Tyr Pro Val Leu Lys Glu

[illegible]

aaatttggtga	atctatgcttt	gaatccaaga	gacatcttg	aattattata	caatttttaa	1023
attcggagct	accattttta	gcatgagattg	ctcagattga	cactgaagaa	tattatgcaa	1083
acaagctttg	ttttaatat	aagcaatccc	caaaaagattt	gagttttctta	gttunaaaatt	1143
tgatcccttt	ccataatgac	actgagttca	tgggatgttc	taactcaattt	catactctgt	1203
gaatattcaa	aagtaataga	atctggcata	tagttttatt	gattcccttag	ccatgggatt	1263
attgaggctt	tcacatatca	gtgatttttaa	aataccagtg	ttttttgctc	tcatttctat	1323
gtattcagtc	ccaggattttt	gaatggtttt	ctaataact	gacatctgca	tttaattttc	1383
agaaattaaa	tttaattttca	tgtctgaatg	ctgtaattcc	atttatatac	tttaagtaaa	1443
caataaagat	tactacaatt	aaacacatag	ttccagtttc	tatggccttc	ccctcccacc	1503
ttctattata	aattaattttt	atctgggtatt	tttaaacatt	taaaaattta	tcctcagata	1563
tcagcatatg	cccaatttatg	cccaatgaaa	cttaataagc	atttaatttt	ccatcataca	1623
ttatagocaa	ggcctatata	ctatatataa	ttttggattt	gtttaatctt	acaggctggt	1683
ttccattgta	tcaccaagtg	gaagttcaag	acggcatcaa	acaaaacaag	gatgtttaca	1743
gacatatgca	aagggtccagg	atatctatcc	tcagtatat	gttaatgctt	aataacaagt	1803
aatccaaaca	gcattaaagg	ccaaatctgt	cccttttccc	ctgaattccct	tacagcatgt	1863
ttatattaca	agccattcag	ggacaaaaga	accttgacta	ccccactgtc	tactaggaac	1923
aaacaaaacag	caagcaaaat	tcactttgaa	agcaccagtg	gttccattac	attgacaact	1983
actaccaaga	ttcagtagaa	aataagtgtc	caacaactaa	tcagatttac	aatatgattt	2043
attgcacat	aaaattccaa	caattccagat	tatttttaatt	catctcagcc	acacctgtaa	2103
atgggcaca	ttacttttta	caatccatcc	ctctcttttt	ctagaataa	tttcaatttt	2163
atggaggta	caggaggagg	aaatttgcaa	ctgtcttttg	acaaataaatt	aggttatata	2223
ttctgggtgta	gagataggat	gttgaaaagct	gcctctctat	caccagtgta	gaaattaaga	2283
gtagtacaat	acatgtacac	tcaaattttg	catacagttt	ttgtgtaaaac	tcattgtgca	2343
catctttctat	ttcaaaaaaa	aaaaataaaaa	caaaaataaa	atgttwawaa	mwwaaaaaa	2403

Figure 1. The effect of the concentration of the H_2O_2 solution on the amount of the H_2O_2 consumed in the reaction of the H_2O_2 with the Fe^{2+} ion. The concentration of the Fe^{2+} ion was 1.0×10^{-2} mol/L. The concentration of the H_2O_2 solution was 0.001, 0.002, 0.004, 0.006, 0.008, 0.010, 0.012, 0.014, 0.016, 0.018, 0.020, 0.022, 0.024, 0.026, 0.028, 0.030, 0.032, 0.034, 0.036, 0.038, 0.040, 0.042, 0.044, 0.046, 0.048, 0.050, 0.052, 0.054, 0.056, 0.058, 0.060, 0.062, 0.064, 0.066, 0.068, 0.070, 0.072, 0.074, 0.076, 0.078, 0.080, 0.082, 0.084, 0.086, 0.088, 0.090, 0.092, 0.094, 0.096, 0.098, 0.100 mol/L. The concentration of the Fe^{2+} ion was 1.0×10^{-2} mol/L. The concentration of the H_2O_2 solution was 0.001, 0.002, 0.004, 0.006, 0.008, 0.010, 0.012, 0.014, 0.016, 0.018, 0.020, 0.022, 0.024, 0.026, 0.028, 0.030, 0.032, 0.034, 0.036, 0.038, 0.040, 0.042, 0.044, 0.046, 0.048, 0.050, 0.052, 0.054, 0.056, 0.058, 0.060, 0.062, 0.064, 0.066, 0.068, 0.070, 0.072, 0.074, 0.076, 0.078, 0.080, 0.082, 0.084, 0.086, 0.088, 0.090, 0.092, 0.094, 0.096, 0.098, 0.100 mol/L.

The Asp Thr Ser Glu Asp Ser Val Glu Asp Glu Leu Glu Met Ala Thr
 35 40 45

Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys
50 55 60

Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Glu
65 70 75 80

Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr Ser
85 90 95

Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe
103 105 110

Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe
115 120 125

Ile Lys Gly Leu Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys Leu
130 135 140

Asn Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Thr
145 150 155 160

Lys Glu Glu Met Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly
165 170 175

Lys Cys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val
180 185 190

Glu Thr Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Val Val Thr
195 200 205

Ile Asp Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn Ile Met Arg
 210 215 220

Sex Net Gm. Len. No. Sds. Ass. Val. 100
240 200 200

<210> 50
<211> 1591
<212> RNA
<213> Salmon SR

1. *Journal of the American Medical Association*, 1997; 277: 1033-1036.

[illegible]

[illegible][illegible][illegible]

gga ctg caa aca gtg ggt att gtt ggg att ata tgt gca tct ctg aag 339
Gly Leu Gln Thr Val Gly Ile Val Val Ile Ile Cys Ala Ser Leu Lys
10 15 20 25

ctg ctt cat ttg ctg gga ctg att gat ttt tog gaa gac agc gtg gaa 387
Leu Leu His Leu Leu Gly Leu Ile Asp Phe Ser Glu Asp Ser Val Glu
30 35 40

gat gaa ctg gag atg gcc act gtc agg cat cgg cct gag gcc ctt gag 435
Asp Glu Leu Glu Met Ala Thr Val Arg His Arg Pro Glu Ala Leu Glu
45 50 55

ctt ctg gaa gcc cag agc aaa ttt acc aag aaa gag ctt cag atc ctt 483
Leu Leu Glu Ala Gln Ser Lys Phe Thr Lys Lys Glu Leu Gln Ile Leu
60 65 70

tac aga gga ttt aag aac gaa tgc ccc agt ggt gtt gtt aat gaa gaa 531
 Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val Val Asn Glu Glu
 75 80 85

acc ttc aaa gag att tac tgc cag ttc ttt cca cag gga gac tct aca 579
Thr Phe Lys Glu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Thr
90 95 100 105

aca tat gca cat ttt ctg ttc aat gog ttt gat acg gac cac aat gga 627
Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Thr Asp His Asn Gly
110 115 120

get gtg agt ttc gag gat ttc atc aaa ggt ctt tcc att ttg ctc cgg 675
Ala Val Ser Phe Glu Asp Phe Ile Lys Gly Leu Ser Ile Leu Leu Arg
125 130 135

Gly Ala Gln Cys Asn Lys Leu Asp Trp Ala Phe Asn Leu Tyr Asp Ile 723
Gly Thr Val Gln Glu Lys Leu Asn Trp Ala Phe Asn Leu Tyr Asp Ile
 140 145 150

Met Asn Gln Arg Leu Ala Asn Asn Gln Gln Arg Ser Gln Ala Arg Asn
 Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys
 155 160 165

Gca ata tac gac atg atg ggt aaa tgt asa tat cct gtr cta aaa gaa 319
 Ala ile Tyr Asp Met Met Gly Lys Cys Thr Tyr Pro Val Leu Lys Glu
 170 175 180 185

111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735

14	15	16	17	18
Lys Glu Glu Ser	Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly			
165	170	175		
Lys Lys Thr Tyr	Pro Val Leu Lys Glu Asp Ala Leu Arg Gln His Val			
180	185	190		
Glu Thr Phe Phe	Gln Ala Val Phe His Cys Ile Ile Lys Trp Lys Phe			
195	200	205		
Lys Thr Ala Ser Asn Lys Thr Arg Met Phe Thr Asp Ile Cys Lys Gly				
210	215	220		
Ser Gly Tyr Leu Ser Ser Ser Ile Cys				
225	230			

<210> 52
 <211> 2051
 <212> DNA
 <213> Rattus sp.

<220>
 <221> CDS
 <222> (85)..(1305)

<400> 52
 ggtggagata agcaactcaat ggggtgctgc cctggctctg cagagaacaa ggaaagcttc 60

cctgcagggc tctcagctgc caaaa atg aac ggc gtg gaa ggg aac aac gag 111
 Met Asn Gly Val Glu Gly Asn Asn Glu
 1 5

ctc cct ctc gct aac acc tgg acc tcc gcc ctt gtc ccg gaa gat ctg 159
 Leu Pro Leu Ala Asn Thr Ser Thr Ser Ala Leu Val Pro Glu Asp Leu
 10 15 20 25

gat ctg aag caa gac cag ccg ctc agc gag gaa act gac acg gtg cgg 207
 Asp Leu Lys Gln Asp Gln Pro Leu Ser Glu Glu Thr Asp Thr Val Arg
 30 35 40

gag atg gag gct gca ggt gag gcc ggt gag gaa ggc gag tcc ccc 255
 Glu Met Glu Ala Ala Gly Val Ala Gly Ala Glu Gly Gly Ala Ser Pro
 45 50 55

gat tgg gag cac tgc gac ccc cag ctc tgc ctc cga gtg gct gag aat 303
 Asp Ser Glu His Cys Asp Pro Gln Leu Cys Leu Arg Val Ala Glu Asn
 60 65 70

ggt tgt gtt ggt gta ggt gta gag ggt ctt gag tat ggt ctg tat tta 351
 Gly Cys Ala Ala Ala Ala Gly Glu Gly Leu Glu Asp Gly Leu Ser Ser

aat aat tat ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt ttt 447
 Asn Asn Asn Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe

447
Lys Thr Leu Gln Ala Ser Gly Ala Val Gly Leu Gly Ser Gln Met Met
137 141 145

843
Pro Gly Pro Lys Lys Thr Lys Val Met Thr Thr Lys Gly Ala Ile Ser
140 145 150

1391
Ala Thr Thr Gly Lys Glu Gly Glu Ala Gly Ala Ala Met Gln Glu Lys
135 160 165

639
Lys Gly Val Gln Lys Glu Lys Lys Ala Ala Gly Gly Gly Lys Asp Glu
170 175 180 135

687
Thr Arg Pro Arg Ala Pro Lys Ile Asn Asn Cys Met Asp Ser Leu Glu
190 195 200

735
Ala Ile Asp Gln Glu Leu Ser Asn Val Asn Ala Gln Ala Asp Arg Ala
205 210 215

783
Phe Leu Gln Leu Glu Arg Lys Phe Gly Arg Met Arg Arg Leu His Met
220 225 230

831
Gln Arg Arg Ser Phe Ile Ile Gln Asn Ile Pro Gly Phe Trp Val Thr
235 240 245

879
Ala Phe Arg Asn His Pro Gln Leu Ser Pro Met Ile Ser Gly Gln Asp
250 255 260 265

927
Glu Asp Met Met Arg Tyr Met Ile Asn Leu Glu Val Glu Glu Leu Lys
270 275 280

975
His Pro Arg Ala Gly Cys Lys Phe Lys Phe Ile Phe Gln Ser Asn Pro
285 290 295

1023
Tyr Phe Arg Asn Glu Gly Leu Val Lys Glu Tyr Glu Arg Arg Ser Ser
300 305 310

1071
Gly Arg Val Val Ser Leu Ser Thr Pro Ile Arg Trp His Arg Gly Gln
315 320 325

110
Pro Ile Thr Asn Tyr Thr Ser Arg His Ser Leu Ile Gln Thr Arg Arg
325 330 335

115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738

Ala Gly Pro Leu Ser Pro Ala Lys Pro Lys Thr Leu Glu Ala Ser Gly
115 125

Ala Val Gly Ileu Gly Ser Gln Met Met Pro Gly Pro Lys Lys Thr Lys
130 135 140

Val	Met	Thr	Thr	Lys	Gly	Ala	Ile	Ser	Ala	Thr	Thr	Gly	Lys	Glu	Gly
145					150					155					160

Glu Ala Gly Ala Ala Met Gln Glu Lys Lys Gly Val Gln Lys Glu Lys
165 170 175

Lys Ala Ala Gly Gly Gly Lys Asp Glu Thr Arg Pro Arg Ala Pro Lys
180 185 190

Ile Asn Asn Cys Met Asp Ser Leu Glu Ala Ile Asp Gln Glu Leu Ser
195 200 205

Asn Val Asn Ala Gln Ala Asp Arg Ala Phe Leu Gln Leu Glu Arg Lys
210 215 220

Phe Gly Arg Met Arg Arg Leu His Met Glr Arg Arg Ser Phe Ile Ile
225 230 235 240

Gln Asn Ile Pro Gly Phe Trp Val Thr Ala Phe Arg Asn His Pro Gln
245 250 255

Leu Ser Pro Met Ile Ser Gly Gln Asp Glu Asp Met Met Arg Tyr Met
260 265 270

Ile Asn Leu Glu Val Glu Glu Leu Lys His Pro Arg Ala Gly Cys Lys
275 280 285

Phe Lys Phe Ile Phe Gln Ser Asn Pro Tyr Phe Arg Asn Glu Gly Leu
290 295 300

Val Lys Glu Tyr Glu Arg Arg Ser Ser Gly Arg Val Val Ser Leu Ser
294 312 330 348

[illegible]

Arg Asn Arg Glu Gly Asn Thr Ile Pro Ser Phe Phe Asn Trp Phe Ser
340 345 350

Asp His Ser Leu Leu Glu Phe Asp Arg Ile Ala Glu Ile Ile Lys Gly

400

<210> 54
 <211> 414-
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (88)..(1329)

<400> 54
 ggggtggtgc tagaegtttc gggcagagct cggcggctgc ggaggacaag gaactctccc 60
 tctcccaacta gtctgaacttc ttccaaa atg agc ggc ctg gat ggg ggc aac aag 114
 Met Ser Gly Leu Asp Gly Gly Asn Lys
 1 5
 ctg cct ctg gcc caa acc ggc gcc ctg gct gct ccc gac caa gcc tca 162
 Leu Pro Leu Ala Gln Thr Gly Gly Leu Ala Pro Asp His Ala Ser
 10 15 20 25
 gga gat ccg gac cta gac cag tgc caa ggg ctg cgt gaa gaa acc gag 210
 Gly Asp Pro Asp Leu Asp Gln Cys Gln Gly Leu Arg Glu Glu Thr Glu
 30 35 40
 gcg aca cag gtg atg gcc aac aca ggt ggg ggc agc ctg gag acc gtt 258
 Ala Thr Gln Val Met Ala Asn Thr Gly Gly Gly Ser Leu Glu Thr Val
 45 50 55
 gcg gag ggg ggt gca tcc cag gat cct gtc gac tgt ggc ccc gcg ctg 306
 Ala Glu Gly Gly Ala Ser Gln Asp Pro Val Asp Cys Gly Pro Ala Leu
 60 65 70
 cgc gtc cca gtt gcc ggg agt cgc ggc ggt gca gcg acc aaa gcc ggg 354
 Arg Val Pro Val Ala Gly Ser Arg Gly Gly Ala Ala Thr Lys Ala Gly
 75 80 85
 cag gag gat gct cca cct tct acg aaa ggt ctg gaa gca gcc tct gcc 402
 Gln Glu Asp Ala Pro Pro Ser Thr Lys Gly Leu Glu Ala Ala Ser Ala
 90 95 100 105
 gct gag ggt gct gct agt agc caa aaa cct gct ggt cag ctt gga gag 450
 Ala Glu Ala Ala Asp Ser Ser Gln Lys Asn Gly Cys Gln Leu Gly Glu
 110 115 120
 ccc cgt gcc cct gct ggg cag aag gct cta gaa gcc tgt ggc gca ggg 498
 Pro Arg Gly Pro Ala Gly Gln Lys Ala Leu Glu Ala Cys Gly Ala Gly
 125 130 135
 ggc ttg ggt tct cag atg ata ccc gcc aag aag cct aag gaa gtg aat 546
 Gly Tyr Gly Thr Cys Met Ala Ser gcc aag aag cct aag gaa gtg aat
 140 145 150
 ggc ttg ggt tct cag atg ata ccc gcc aag aag cct aag gaa gtg aat 546
 Gly Tyr Gly Thr Cys Met Ala Ser gcc aag aag cct aag gaa gtg aat
 150 155 160

tttttttttt tttttttt tttttttttt tttttttt tttttttt tttttttt
 agaatatata tttttttt tttttttttt tttttttt tttttttt agaatatata
 tttttttt tttttttt tttttttttt tttttttt tttttttt tttttttt
 aaaagttatg agaatataatg agaatgtgtgt ttgttttttt ttgaaatgtt aatgtttaa
 aacctgtatg atcaatgtgt ggaggggagg taactgtgt gtctctatagg gaaataggggt
 tgggggtttaa atagcatgtt ttgaggaaga ttttctttca atttttctta agtaactgaa
 ttcaccagtta gattttttgt aacaaaaatgt aagtctatgt tttctctcaa ttatctatgg
 agtgaccttt atattgtgtg agagattaatg gtatatgtct cttatgtctc ttgtttttgag
 taaaatccat ttctttttct tgttttcagcc tatgacaaaa ttgatgttta caggcctgtt
 tttgtcttat aattgacaa atgtgcaaaa atacaaaatt tgtgtctgtt gcaatgatga
 gaattcagtg aatattcatt aatgtatttag cttgtttttg totctgttca tatatggctc
 tattcttata aataaattt gaatgtgata tttcaatagt ctgaatatatt taacaaattat
 agctatgtct tgtgaaaaata acctcaaaaa gaaaaataacg actctgtttg cttacttgat
 attttttgct ctagtaatgt acttgacatt tatgttctta agcagtgtaa gtaccagtag
 aatttctctg tcaaaatcaa tgaatcattta gtaactttgt cttctctccat gtgtttgaag
 gaaaaataaa gtgtcactac cgtattttctt gttttcatca aaaaataaaa ataatttaaa
 aaacaaaaaa aaaaaaaaaa

```
<210> 55
<211> 414
<212> PRT
<213> Homo sapiens
```

```

<400> 55
Met Ser Gly Leu Asp Gly Gly Asn Lys Leu Pro Leu Ala Gln Thr Gly
  1          5          10          15
Gly Leu Ala Ala Pro Asp His Ala Ser Gly Asp Pro Asp Leu Asp Gln
  20          25          30          35
Cys Gln Gly Leu Arg Glu Glu Thr Glu Ala Thr Gln Val Met Ala Asn
  35          40          45
Thr Gly Gly Gly Ser Leu Glu Thr Val Ala His Gly Gly Ala Ser Gln
  50          55          60

```

Gln Lys Asn Gly Lys Gln Leu Gly Ala Ile Asn Gly Ile Ala Gly His
111 121 127

Lys Ala Leu Ala Ala Lys Gly Ala Gly Gly Leu Gly Ser Gln Met His
130 135 140

Pro Gly Lys Lys Ala Lys Glu Val Thr Thr Lys Lys Arg Ala Ile Ser
145 150 155 160

Ala Ala Val Glu Lys Glu Gly Glu Ala Gly Ala Ala Met Glu Glu Lys
165 170 175

Lys Val Val Gln Lys Glu Lys Lys Val Ala Gly Gly Val Lys Glu Glu
180 185 190

Thr Arg Pro Arg Ala Pro Lys Ile Asn Asn Cys Met Asp Ser Leu Glu
195 200 205

Ala Ile Asp Gln Glu Leu Ser Asn Val Asn Ala Gln Ala Asp Arg Ala
210 215 220

Phe Leu Gln Leu Glu Arg Lys Phe Gly Arg Met Arg Arg Leu His Met
225 230 235 240

Gln Arg Arg Ser Phe Ile Ile Gln Asn Ile Pro Gly Phe Trp Val Thr
245 250 255

Ala Phe Arg Asn His Pro Gln Leu Ser Pro Met Ile Ser Gly Gln Asp
260 265 270

Glu Asp Met Leu Arg Tyr Met Ile Asn Leu Glu Val Glu Glu Leu Lys
275 280 285

His Pro Arg Ala Gly Cys Lys Phe Lys Phe Ile Phe Gln Gly Asn Pro
290 295 300

Tyr Phe Arg Asn Glu Gly Leu Val Lys Glu Tyr Glu Arg Arg Ser Ser
305 310 315 320

Gly Arg Val Val Ser Leu Ser Thr Pro Ile Arg Trp His Arg Gly Gln
325 330 335

Asp Pro His Ala His Ile His Arg Asn Arg Gln Gly Asn Thr His Ile
340 345 350

Ser Phe Phe Asn Trp Phe Ser Asp His Ser Leu Leu Glu Phe Asp Arg
355 360 365

Ile Ala Glu Ile Ile Lys Gly Glu Leu Trp Pro Asn Pro Leu Gln Tyr
370 375 380

His Ile Val Val Val Ala Asn Ser His Asn Ile Val Ser Gly
390 400 405

4121 - 1047
 4121 - 1048
 4121 - 1049 sp.

4121 -
 4121 - 1048
 4122 - 1049 (1049)

<400> 56

ctg aaa ggg gag agg ccc agg ggg gtg aac tcc acc tgg agt gac ttc	48
Leu Lys Gly Ala Arg Pro Arg Val Val Asn Ser Thr Cys Ser Asp Phe	
1 5 10 15	
aac cat ggc tca gct ctg cac atc gct gcc tgg aat ctg tgc ctg ggc	96
Asn His Gly Ser Ala Leu His Ile Ala Ala Ser Asn Leu Cys Leu Gly	
20 25 30	
gcc gcc aaa tgt tta ctg gag cat ggt gcc aac cca gcc ctg agg aat	144
Ala Ala Lys Cys Leu Leu Glu His Gly Ala Asn Pro Ala Leu Arg Asn	
35 40 45	
cga aaa gga cag gta cca gcc gaa gtg gtc cca gac ccc atg gac atg	192
Arg Lys Gly Gln Val Pro Ala Glu Val Val Pro Asp Pro Met Asp Met	
50 55 60	
tcc ctt gac aag gca gag gca gcc ctg gtg gcc aag gaa ttg cgg acg	240
Ser Leu Asp Lys Ala Glu Ala Ala Leu Val Ala Lys Glu Leu Arg Thr	
65 70 75 80	
ctg cta gaa gag gct gtg cca ctg tcc tgc acc ctt cct aaa gtc aca	288
Leu Leu Glu Glu Ala Val Pro Leu Ser Cys Thr Leu Pro Lys Val Thr	
85 90 95	
cta ccc aac tat gac aac gtc cca gcc aat ctc atg ctc agc gcc ctg	336
Leu Pro Asn Tyr Asp Asn Val Pro Gly Asn Leu Met Leu Ser Ala Leu	
100 105 110	
ggc ctg cgt cta gga gac cga gtg ctc ctc gat gcc cag aag acg gcc	384
Gly Leu Arg Leu Gly Asp Arg Val Leu Leu Asp Gly Gln Lys Thr Gly	
115 120 125	
aag ctg agg ttc tgt ggt aac acc gag ttc gcc agt gcc cag tgg gtg	432
Thr Leu Arg Phe Cys Gly Thr Thr Glu Phe Ala Ser Gly Gln Trp Val	
130 135 140	
ggc gtg gag cta gat gaa cgg gaa gcc aag aac gac gcc agt gtt ggt	480
Gly Val Glu Leu Asp Glu Pro Glu Gly Lys Asn Asp Gly Ser Val Gly	
145 150 155 160	
ggt gtc agg tac ttc atc ttc cct ccc aag cag ggt ctc ttt gca tct	528
Gly Val Arg Tyr Phe Ile Cys Pro Pro Lys Gln Gly Leu Phe Ala Ser	
165 170 175	
ctg acc ccc acc acc acc acc acc acc acc acc acc acc acc acc acc	576
Ser Thr Pro Arg Thr Pro Arg Met Asp Phe Ser Ala Val Thr Gly Lys	

atggaatg atggaatg atggaatg atggaatg atggaatg atggaatg 1
 agtgcata ttgggaacaa ggaagaaa atggaatg atggaatg atggaatg 2
 tgaacata caaactaat ggaagaaa atggaatg atggaatg atggaatg 3
 gataactaat atgtgcaggg aacaggggt atagaggac caaactaat atggaatg 43-1
 ctccaatcct cctttctgggt acaggtcctaa caaactaat atggaatg atggaatg 2441
 gaattcacag caactggggc agactaacag atggaagggag aacttgaggg aacttgagggt 2501
 ccagagcaga cctggggggc tgaccaccaa ggaagagctca gaactggggc ttaactgcct 2561
 gtccctaaac tcagcatgac tctgtctctc ttaataaag acgtttctat gcaaaaaaaaa 2621
 aaaaaaaaaa aaaaaaaaaa aa 2643

<210> 57

<211> 267

<212> PRT

<213> Rattus sp.

<400> 57

Leu Lys Gly Ala Arg Pro Arg Val Val Asn Ser Thr Cys Ser Asp Phe
 1 5 10 15

Asn His Gly Ser Ala Leu His Ile Ala Ala Ser Asn Leu Cys Leu Gly
 20 25 30

Ala Ala Lys Cys Leu Leu Glu His Gly Ala Asn Pro Ala Leu Arg Asn
 35 40 45

Arg Lys Gly Gln Val Pro Ala Glu Val Val Pro Asp Pro Met Asp Met
 50 55 60

Ser Leu Asp Lys Ala Glu Ala Ala Leu Val Ala Lys Glu Leu Arg Thr
 65 70 75 80

Leu Leu Glu Glu Ala Val Pro Leu Ser Cys Thr Leu Pro Lys Val Thr
 85 90 95

Leu Pro Asn Tyr Asp Asn Val Pro Gly Asn Leu Met Leu Ser Ala Leu
 100 105 110

Gly Leu Arg Leu Gly Asp Arg Val Leu Leu Asp Gly Gln Lys Thr Gly
 115 120 125

Thr Leu Arg Phe Cys Gly Thr Thr Glu Phe Ala Ser Gly Gln Trp Val
 130 135 140

Val Ser Lys Val Ser Lys Ala Val Asn Ala Pro Leu Ser Ser Val Thr

Leu Gly Ser Leu Gln Gln Arg Gln Gly Ala Lys Ala Glu Val Gly Asp
 681 682 683 684 685 686 687 688 689 690 691 692 693 694

Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Tyr Glu
245 250 255

Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
260 265

<210> 58
<211> 2929
<212> DNA
<213> Rattus sp.

```
<220>  
<221> CDS  
<222> (1)..(810)
```

```
<400> 58
gct gac tct acc tct aga tgg gct gag gcc ctg aga gaa atc tct ggt      48
Ala Asp Ser Thr Ser Arg Trp Ala Glu Ala Leu Arg Glu Ile Ser Gly
      1           5           10           15
```

cgc tta gct gaa atg cct gca gat agt gga tac cct gca tac ctt ggt 96
Arg Leu Ala Glu Met Pro Ala Asp Ser Gly Tyr Pro Ala Tyr Leu Gly
 20 25 30

gac cga ctg gct tct ttc tat gag cga gca ggc aga gtg aaa tgt ctt 144
Ala Arg Leu Ala Ser Phe Tyr Glu Arg Ala Gly Arg Val Lys Cys Leu
35 40 45

gga aac cct gag aga gaa ggg agt gtc agc att gta gga gca gtt tct 192
Gly Asn Pro Glu Arg Glu Gly Ser Val Ser Ile Val Gly Ala Val Ser
50 55 60

Ala Ser Gly Gly Glu His Leu Val Gln Gln Glu Ala Ser Ser Ser Ser Gly Gly 24
 Pro Pro Gly Gly Asp Ile Ser Asp Pro Val Thr Ser Ala Thr Leu Gly
 65 70 75

att gtt cag gtg ttc tgg ggc ttg gat aag aag cta got cag ggc aag 288
Ile Val Gln Val Phe Trp Gly Leu Asp Lys Lys Leu Ala Gln Arg Lys
35 90 95

Cys His Arg Asp Gln Asn Lys Glu Ala Arg Leu Arg Asn Thr Asn Asp
 His Phe Thr Ser Val Asp Trp Leu Phe Ser Thr Ser Lys Tyr Met Arg

[illegible]

tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 171
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 177
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 183
 agtttccat agtttccat agtttccat agtttccat agtttccat 189
 aaagaaaaaa aagatogatt ttgtctctgc tgttttgggt tgttttccat ataattccat 1950
 atttgcataa agaggctcgc ttctgagaga ttggagatcg tgttccctct tccctctcgc 2010
 ggggtgataat gctggcgcca tctacccctc tcaggagggg aaggggattg aacatggcta 2070
 acactctcaa gtacacaagg gtaacgacaa agtatttatt ttaagccttg gtatgttgtt 2130
 taaattatta ggtgggtgcat ttcttatggt cttttgggta gacatagtat acacttcaga 2190
 tgtaattgtt aaatccctgc tagtgcattg ctacacgata gactgctatt caagaaggat 2250
 attcttccac ataacaattt aaaaaacttt aaatccgata tggattatgc aatgacttgt 2310
 tgagaggttg attaacgggtg ctgcttaate agtttgcctc caatatggct tctatccag 2370
 aagccctgac tagtggagat gagaaagatt tcaaaacctg tctgcctaca cctaccagca 2430
 acctaggctt gtgacacaga tgaatgatcc caagaaaacta cttgaccaag tgtgttttgt 2490
 tgtcctggat ttgagatgtg cgttcttctc cctctgaga ctgttgatgt atgagtgtga 2550
 agaagttaca gaaacaaagg tcagattttc acggtaactt tccctctgac cacactgtag 2610
 agtttcagat tgttccactga tagtgcctct ttctgaagga tgtgttaaaa tatagcagtc 2670
 tttttaaaaag attatgcagt tctctattta ttgtctgtg cctggctcta agtgacgcgc 2730
 gttaaacaag ttccatatgt atttttccag tgttaaatct cctacccatg ccttttggaa 2790
 agctccatcc tgaacaatga atagaagagg ctatataaat tgcctcctta tctttaagat 2850
 ttcactatct ttatgttaag agtaatgfat aattattaaa atctatgaaa aataaaaaagt 2910
 ttatttaaat ttatgagatc 2929

<210> 39

<211> 270

<212> PRT

<213> Rattus sp.

<410> 59

Ala Asp Ser Thr Ser Arg Trp Ala Glu Ala Leu Arg Glu Ile Ser Gly

Ala Arg Ile Ala Ser Ile Tyr Arg Arg Ala Tyr Arg Val Tyr Tyr Ile

His Pro Gly Gly Asp Phe Ser Asp 1: Val Thr Ser Ala Thr Leu Gly
 10 20 30 40 50 60 70 80 90
 Ile Val Ala Val Phe Trp Gly Leu Asp Lys Lys Leu Ala His Arg Lys
 25 35 45 55 65 75 85 95
 His Ile Pro Ser Val Asn Trp Leu Ile Ser Tyr Ser Lys Tyr Met Arg
 100 110 120 130 140 150 160 170 180
 Ala Leu Asp Glu Tyr Tyr Asp Lys His Phe Thr Glu Phe Val Pro Leu
 115 125 135 145 155 165 175 185 195
 Arg Thr Lys Ala Lys Glu Ile Leu Gln Glu Glu Glu Asp Leu Ala Glu
 130 140 150 160 170 180 190 200 210
 Ile Val Gln Leu Val Gly Lys Ala Ser Leu Ala Glu Thr Asp Lys Ile
 145 155 165 175 185 195 205 215 225
 Thr Leu Glu Val Ala Lys Leu Ile Lys Asp Asp Phe Leu Gln Gln Asn
 165 175 185 195 205 215 225 235 245
 Gly Tyr Thr Pro Tyr Asp Arg Phe Cys Pro Phe Tyr Lys Thr Val Gly
 180 190 200 210 220 230 240 250 260 270
 Met Leu Ser Asn Met Ile Ser Phe Tyr Asp Met Ala Arg Arg Ala Val
 195 205 215 225 235 245 255 265 275 285
 Glu Thr Thr Ala Gln Ser Asp Asn Lys Ile Thr Trp Ser Ile Ile Arg
 210 220 230 240 250 260 270 280 290 300
 Glu His Met Gly Glu Ile Leu Tyr Lys Leu Ser Ser Met Lys Phe Lys
 225 235 245 255 265 275 285 295 305 315
 Asp Pro Val Lys Asp Gly Glu Ala Lys Ile Lys Ala Asp Tyr Ala Gln
 245 255 265 275 285 295 305 315 325 335
 Leu Leu Glu Asp Met Gln Asn Ala Phe Arg Ser Leu Glu Asp
 260 270 280 290 300 310 320 330 340 350

<210> 60
 <211> 1459
 <212> DNA
 <213> Rattus sp.

<220>
 <221> CDS
 <222> (1)..(1053)
 <400> 60

His Pro Gly Gly Asp Phe Ser Asp 1: Val Thr Ser Ala Thr Leu Gly
 10 20 30 40 50 60 70 80 90
 Ile Val Ala Val Phe Trp Gly Leu Asp Lys Lys Leu Ala His Arg Lys
 25 35 45 55 65 75 85 95

141 211 212 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 128

Ser Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg Arg 460
 Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln Glu Leu Cys Arg Gln
 305 310 315 320

cgc atc gtg gcc gcc gtg ggt cgc gag aac ctg gca cgc atc cct ctt 1008
 Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu Ala Arg Ile Pro Leu
 325 330 335

aac cag gta ctc cgt gac tac ctg agt tcc ttc ccc ttc cag atc 1053
 Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe Pro Phe Gln Ile
 340 345 350

```

tgacccgctg ccgccgtgcc cgcagcatta agtgggagcg ccttattatt tcttattatt 1113
aattattatt attttctctg aaccacgtgg gagccctccc cgcctaggtc ggagggagtg 1173
ggtgtggagg gtgagatgcc tcccacttct ggtcggagac cttatccgcg ctctcggggg 1233
gcctcccttc ctggtgctcc ctcccggtcc cctcggttgt agcagcttgt gtctggggcc 1293
aggacctgaa ctccacgctt acctctccat gtttacatgt tccagttatc ttgcacaaa 1353
ccaggggtgg gggagggctc ctggttccat tttctctctg tgcagaatat tctattttat 1413
attttacat ccagtttaga taataaaact tattatgaaa gttttttttt taaagaaaaa 1473
aaaaaaaaa aaaaaa
1489

```

```
<210> 61
<211> 351
<212> PRT
<213> Rattus sp.
```

Ala Arg Leu Pro Ala Pro Glu His Ala Arg Glu His Pro Leu Leu Ser
 1 5 10 15
 Gly Pro Glu Pro Gly Ser Ser Ala Arg Val Pro Val Pro Gly Val Ala
 20 25 30
 Ser Arg Arg Glu Pro Arg Gly Gly Lys Pro Pro Ser Gly Asp Gly Leu
 35 40 45

Asp Ile Ser Leu Leu Arg Val Asn Trp Ile Ala Tyr Ala Ile Asn Ile
100 105 110

Pro Gly Ser Leu Pro Leu Ser Phe Pro Ser Ala Gln Pro Asn Thr Leu
115 120 125

Trp Pro Thr Pro Pro Ala Gly Pro Ser Ser Arg Met Val Ala Arg Asn
130 135 140

Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala Ser Glu Pro Arg Arg
145 150 155 160

Arg Pro Glu Pro Ser Ser Ser Ser Ser Ser Ser Pro Ala Ala Pro
165 170 175

Ala Arg Pro Arg Pro Cys Pro Val Val Pro Ala Pro Ala Pro Gly Asp
180 185 190

Thr His Phe Arg Thr Phe Arg Ser His Ser Asp Tyr Arg Arg Ile Thr
195 200 205

Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe Tyr Trp Gly Pro Leu
210 215 220

Ser Val His Gly Ala His Glu Arg Leu Arg Ala Glu Pro Val Gly Thr
225 230 235 240

Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys Phe Phe Ala Leu Ser
245 250 255

Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg Val His Phe Gln Ala
260 265 270

Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr Phe Asp Cys Leu Phe
275 280 285

Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg Arg Met Leu Gly Ala
290 295 300

Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln Glu Leu Cys Arg Gln
305 310 315 320

Arg Ile Val Ala Ala Val Gly Arg His Asn Leu Ala Arg Ile Phe Leu
325 330 335

Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe Pro Phe Gln Ile
340 345 350

210 62

11/11/11
11/11/11

<220>
 <221> CDS
 <222> (52)..(336)
 <400> 64

```

cttccaaaga ctgcagcgcc tcaggggccc ggtttccaaca gattottcaa a atg cca 57
                                         Met Pro
                                         1

tcc caa atg gag cat gcc atg gaa acc atg atg ott aca ttt cac agg 105
Ser Gln Met Glu His Ala Met Glu Thr Met Met Leu Thr Phe His Arg
                                         10
                                         15

ttt gca ggg gaa aaa aac tac ttg aca aag gag gac atg aga gtg ctc 153
Phe Ala Gly Glu Lys Asn Tyr Leu Thr Lys Glu Asp Leu Arg Val Leu
    20                25                30

atg gaa agg gag ttc cct ggg ttt ttg gaa aat caa aag gac cct ctg 201
Met Glu Arg Glu Phe Pro Gly Phe Leu Glu Asn Gln Lys Asp Pro Leu
    35                40                45                50

gct gtg gac aaa ata atg aaa gac ctg gac cag tgc cga gat gga aaa 249
Ala Val Asp Lys Ile Met Lys Asp Leu Asp Gln Cys Arg Asp Gly Lys
                55                60                65

gtg ggc ttc cag agc ttt cta tca cta gtg ggc ggg ctc atc att gca 297
Val Gly Phe Gln Ser Phe Leu Ser Leu Val Ala Gly Leu Ile Ile Ala
    70                75                80

tgc aat gac tat ttt gta gta cac atg aag cag aag aag taggccaact 346
Cys Asn Asp Tyr Phe Val Val His Met Lys Gln Lys Lys
    85                90                95

ttggactgg taccacacac ttgatgggta ctctaccatg agttcaactg aggaattctg 406

ctctctttt ctctgggga gctcatttt ctctttttt ctctttttt ctctttttt 461

caattcagaa agcagagaaa gaaaagttaa tccattgaca gaggagcttt agagtcttat 516

attgctttgca tccggttgcc ctcaataaag aaagtctttt tttttaagtt ccgaaaaaaaa 586

aaaaaaaaaa aaaa 600
  
```

Met Pro Phe Gln Met Ala His Ala Met Glu Thr Met Met Leu Thr Phe

His Arg Ile Ala Gly Val Lys Asn Tyr Leu Thr Lys Ala Asp Leu Arg
 10 20 30 40 50 60 70 80 90 100
 Val Leu Met His Arg Val Ile His Ile Gly Ile Leu Ala Asn His Lys Arg
 110 120 130 140 150 160 170 180 190 200
 Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp Gln Cys Arg Asp
 210 220 230 240 250 260 270 280 290 300
 Gly Lys Val Gly Phe Gln Ser Phe Leu Ser Leu Val Ala Gly Leu Ile
 310 320 330 340 350 360 370 380 390 400
 Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys Gln Lys Lys
 410 420 430 440 450 460 470 480 490 500

<210> 66

<211> 639

<212> DNA

<213> *Rattus* sp.

<220>

<221> CDS

<222> (1)..(636)

<400> 66

atg gcg tac gcc tat ctc ttc aag tac atc atc atc ggc gac aca ggt 48
 Met Ala Tyr Ala Tyr Leu Phe Lys Tyr Ile Ile Ile Gly Asp Thr Gly
 1 5 10 15
 att ggt aaa tgg tgc tta ttg cta cag ttt aca gac aag agg ttt cag 96
 Val Gly Lys Ser Cys Leu Leu Leu Gln Phe Thr Asp Lys Arg Phe Gln
 20 25 30
 ccg gtg cat gac ctc aca att ggt gta gag ttt ggt gct cga atg ata 144
 Pro Val His Asp Leu Thr Ile Gly Val Glu Phe Gly Ala Arg Met Ile
 35 40 45
 acc att gat ggg aaa cag ata aaa ctc cag atc tgg gat aca gca ggg 192
 Thr Ile Asp Gly Lys Gln Ile Lys Leu Gln Ile Trp Asp Thr Ala Gly
 50 55 60
 cag gag taa ttt cgt tat atc aca att tca tat taa aga ggt aca agg 240
 Gln His Ser Phe Arg Ser Ile Thr Asn Ser Tyr Tyr Arg Gly Ala Ala
 65 70 75
 ggg gct tta cta gtg tat gat att aca agg aga gac acg ttc aac cac 288
 Gly Ala Leu Leu Val Tyr Asp Ile Thr Arg Arg Asp Thr Phe Asn His
 85 90 95
 tgg aca att tgg tta tta tac ggt att cag tat ttt att taa att atg 336
 Leu Thr Thr Trp Leu Gln Asp Ala Arg Gln His Ser Asn Ser Asn Met
 100 105 110 115 120 125 130 135 140 145

tta att att taa taa tta tta tta tta tta tta tta tta tta tta tta 400
 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220

111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 1201 1202 1203 1204 1205 1206 1207 1208 1209 1210 1211 1212 1213 1214 1215 1216 1217 1218 1219 1220 1221 1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735

Arg 110 Asn Asn Ala Ala Asn Gly Ile Lys Ile Gly Ile His His Ala
100 100 100

Ala Thr Asn Ala Ser His Gly Gly Asn Gln Gly Gly Gln His Ala Gly
100 100 100

Gly Gly Cys Cys
210

<210> 68

<211> 816

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (1)..(813)

<223> 68

atg gta gag gta aat gaa tat cgg gta ata ctg act gta tat gta gat 48
Met Val Leu Leu Lys Glu Tyr Arg Val Ile Leu Pro Val Ser Val Asp
1 5 10 15

gag tat caa gtg ggg cag ctg tac tct gtg gct gaa gcc agt aaa aat 96
Glu Tyr Gln Val Gly Gln Leu Tyr Ser Val Ala Glu Ala Ser Lys Asn
20 25 30

gaa act ggt ggt ggg gaa ggt gtg gag gtc ctg gtg aac gag ccc tac 144
Glu Thr Gly Gly Gly Glu Gly Val Glu Val Leu Val Asn Glu Pro Tyr
35 40 45

gag aag gat gat ggc gag aaa ggc cag tac aca cac aag atc tac cac 192
Glu Lys Asp Asp Gly Glu Lys Gly Gln Tyr Thr His Lys Ile Tyr His
50 55 60

ata cag agc aaa gtt ccc aag ttt gtt cga atg ctg gcc cca gaa ggc 240
Leu Gln Ser Lys Val Pro Thr Phe Val Arg Met Leu Ala Pro Glu Gly
65 70 75 80

gcc ctg aat ata cat gag aaa gcc tgg aat gcc tac cct tac tgc aga 288
Ala Leu Asn Ile His Glu Lys Ala Trp Asn Ala Tyr Pro Tyr Cys Arg
85 90 95

att att att aat att att att att att att att att att att att 336
Thr Val Ile Thr Asn Glu Tyr Met Lys Glu Asp Ile Leu Ile Lys Ile
100 105 110

gaa acc tgg cac aag cca gac ctt ggc acc cag gag aat gtg cat aaa 384
Glu Thr Trp His Lys Pro Asp Leu Gly Thr Gln Glu Asn Val His Lys
115 120 125

att att att att att att att att att att att att att att att 432
Ala Arg Arg Arg His Thr Ile Ser Lys Arg Tyr Lys Ala Glu Glu Arg
130 135 140 145

111 Ala Tyr Leu Lys Asn Leu Lys Ile Gly Asn Gly Ser Leu Gly Ser
 101 110 119

112 tgg aat taa gaa att ttc aat ttt aag ttt ttt ttt ttt ttt ttt 606
 Asn Trp Lys Gln Glu Leu Val Asn Gln Lys Asp Cys Pro Tyr Met Cys
 147 148 149

150 gaa tac aaa ctg gtt aat gtc aag ttc aag tgg tgg ggc ttg cag aac 624
 Ala Tyr Lys Leu Val Thr Val Lys Phe Lys Trp Trp Gly Leu Gln Asn
 195 200 205

210 aaa gtg gaa aac ttt ata cat aag caa gag aag cgt ctg ttt aca aac 672
 Lys Val Glu Asn Phe Ile His Lys Gln Glu Lys Arg Leu Phe Thr Asn
 210 215 220

225 ttt cac agg cag ctg ttc tgt tgg ctt gat aaa tgg gtt gat ctg aat 720
 Phe His Arg Gln Leu Phe Cys Trp Leu Asp Lys Trp Val Asp Leu Thr
 225 230 235 240

245 atg gat gac att cgg agg atg gaa gaa gag acg aag aga cag ctg gat 768
 Met Asp Asp Ile Arg Arg Met Glu Glu Glu Thr Lys Arg Gln Leu Asp
 245 250 255

260 gag atg aga caa aag gac ccc gtg aaa gga atg aca gca gat gac tag 816
 Glu Met Arg Gln Lys Asp Pro Val Lys Gly Met Thr Ala Asp Asp
 260 265 270

<210> 69
 <211> 2263
 <212> DNA
 <213> Simian sp.

<400> 69
 cgtctctctc ctccccttctc tctagcagta gccttctctaa tctagtttaa tggctttaca 60
 aagaaagcca ggcagaggag caattctcag tggctgtggt cggaccatga cctagctgac 120
 catcaatttg taagggtctg aaatctatag agttctgata gtcatttggc tttttgataa 180
 attcttgaat tttttgggtt ttttttaatt ttttttata taaggtttat aaattttt 240
 ggagatgggt atgttcagga atgttgctga ggcctttag cttctgggag ccagagatca 300
 atttaccaag aaagagcttc agatccttta cagaggattt aagaacgaat gcccagttgg 360
 tttttttaat gaagaaacct ttaagagat ttaattggat tttttttt agggagattt 420
 ttttttatat tttttttt ttttttaatt tttttttt tttttttt tttttttt 480

ttggtttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 18
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 24
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 30
ttaggttttt ttgaaggttt ttatgttttt ttgttttttt ttatttttttt ttatttttttt 360
aaagatttga gttttttttt ttataatttt ttatttttttt ttatttttttt ttatttttttt 1020
ggatgttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1080
gttttttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1140
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1200
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1260
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1320
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1380
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1440
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1500
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1560
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1620
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1680
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1740
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1800
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1860
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1920
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 1980
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 2040
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 2100
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 2160
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 2220
ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt ttattttttt 2280

ttattttttt
ttattttttt

ttattttttt
ttattttttt

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

<400>

Val Glu Thr Phe Phe Glu Lys Met Asn Lys Asn Lys Asp Gly Val Val

[illegible]